

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 3, 2002, 03:38:42 ; Search time 6582.52 Seconds
(without alignments)
840.674 Million cell updates/sec

Title: US-09-300-482-14

Perfect score: 410
Sequence: 1 cccacgcgtccgcgcatg.....gcaacgcccgtcttcatg 410

Scoring table: IDENTITY_NUC
Gap 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlinu:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl1:*
10: gb_estl2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pin:*
16: em_gss_vrl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	346.8	84.6	530	10	BE363077 DGI_9_F06
2	343.8	83.9	492	10	BI141708 IPL_55_H1
3	323.8	79.0	531	10	BF267183 HV_CEA001
4	323.8	79.0	590	9	AV939826 AV939826
5	323.8	79.0	612	9	AL504224 AL504224
6	323.8	79.0	722	9	BE216705 BE216705
7	323.8	79.0	886	10	BE413061 MCG015_E0
8	322.2	78.6	445	10	BM370860 EBR004_SO
9	321.4	78.4	833	10	BI951719 HVSME000
10	320.6	78.2	466	10	BE471136 BE471136
11	319	77.8	531	10	BI543081 949072H04
12	319	77.8	547	10	BE493869 WHE1276_F
13	319	77.8	823	9	AM448282 BRY_1785
14	317	77.3	875	10	BF630844 HVSME001
15	315.6	77.0	536	10	BI074740 IPL_15_F0
16	314.6	76.7	519	9	AM563648 LGL_245_A
17	313.6	76.5	516	10	BE363025 DGI_9_A10

18	312	76.1	438	10	BG053648 RH122_8_A
19	310.6	75.8	547	9	AV938902 AV938902
20	309	75.4	539	9	AV924281 AV924281
21	307.4	75.0	466	10	BF483000 WHE2313_E
22	307.4	75.0	667	10	BI954565 HVSME001
23	295.2	72.0	743	10	BE414610 SCU011_F0
24	294.4	71.8	473	10	BE657125 OV2_21_B0
25	290.4	70.8	456	10	D24970 RICR2869A_R
26	290.2	70.8	472	10	BE497862 WHE0957_D
27	290.2	70.8	474	10	BE606368 WHE0904_B
28	288.6	70.4	420	10	BF201489 WHE1771_B
29	288.6	70.4	474	10	BE497880 WHE0957_B
30	288.6	70.4	512	10	BE425231 WHE0312_G
31	284	69.3	788	10	BI947260 HVSME1000
32	283.8	69.2	338	10	BG948605 IPL_11_G0
33	281.4	68.6	454	10	BE495944 WHE1259_B
34	281.2	68.6	456	10	BI074623 IPL_13_C0
35	277.4	67.7	781	10	BE414643 SCU011_H1
36	277	67.6	427	9	AU23121 AU23121
37	274	66.8	453	10	BM226433 PIC1_57_A
38	270.6	66.0	446	10	BG262764 WHE0945_A
39	269	65.6	463	9	AM286879 LGL_222_F
40	268.4	65.5	683	10	BG370009 HVSME1002
41	268	65.4	462	9	AM286839 LGL_222_B
42	267	65.1	461	9	AM286858 LGL_222_D
43	266	64.9	460	9	AM677090 DGI_4_B11
44	266	64.9	468	10	BG947868 IPL_6_C11
45	265.8	64.8	467	10	BG053295 RH122_25_

ALIGNMENTS

RESULT 1
BE363077 530 bp mRNA linear EST 20-JUL-2000
LOCUS DGI_9_F06.b1_A002 Dark Grown 1 (DGI) Sorghum bicolor CDNA, mRNA
DEFINITION BE363077
ACCESSION BE363077 GI:9304634
VERSION BE363077.1
KEYWORDS EST.
SOURCE sorghum.
ORGANISM Sorghum bicolor

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 530)

AUTHORS Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt

TITLE 'L.H. database from Sorghum: dark-grown seedlings

JOURNAL Unpublished (2000)

COMMENT Contact: Cordonnier-Pratt MM
Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805

Email: emprat@uga.edu

Sequences have been trimmed to exclude polyA, vector and regions below phred quality 16. The threshold for highest quality sequence is 20.

Seq primer: JEN REV
High quality sequence stop: 453
POLYA-No.

FEATURES
source Location/Qualifiers

1..530
/organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Dark Grown 1 (DGI)"
/note="Organ: 5-day-old dark-grown seedlings; Vector: Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda Zap II. Clones to be sequenced were prepared by mass excision."

BASE COUNT 126 a 132 c 164 g 108 t
ORIGIN

Query Match 84.6%; Score 346.8; DB 10; Length 530;
Best Local Similarity 91.7%; Pred. No. 8.3e-70;
Matches 366; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 12 ggcgtcatgaggcagaaacctgcccctcaacattgcaagaagggtcccatctctgtg 71
DB 91 GCGGTATGGGCGAGAACCTTGGCCCTCAACATTGCAGAGAAAGGCTTCCCATCTCTGTC 150
QY 72 tacaacagagcaaacctccaaggtgacagaccgtgacgctgccaagagcaagaac 131
DB 151 TACAACAGGACAACTCCACAGGTTGATGAGACCGTGACGCGGCAAGGCAAGAGAAAC 210
QY 132 ctcccgctcaagcgttcacatgaccgcgcgtcccttggaagtccattcagaaccacgg 191
DB 211 CTTCCTGTGTACGGCTTCCATGACCTCTGATCTTTGTGAACCTCCATTCAAGAACCGCGT 270
QY 192 gtgtgatacatgctcgtcaagccgcgcgcagttgaccacatcgagagctgcga 251
DB 271 GTTGTCATCATGCTTGTCAAGCGTGCGTGCACACAGTTGACACACATTGGCAGCTCGCA 330
QY 252 gctcaactgagagcagggcgactgcatcgtatgagggaagagtgtagcaagaacag 311
DB 331 GCTCATTGGAGCAGAGGCTGACTGTATGATGAGAGGAATGAGTGTATGAGAACACT 390
QY 312 gagaagagagaaagccatggaagagcgcgcctnctgtatcttgcatggtgtctct 371
DB 391 GAGAGGAGGAGAGAGCCATGAGAGAGCGTGGCTCCTCTATCTTGGAAATGGGCGTCTCT 450
QY 372 ggaagaaagagggtgcccgaagagccgctccttgatg 410
DB 451 GGAGGAGAGAGGAGGTCGCCGACAGCAACCTTGTGATG 489

RESULT 2
LOCUS B1141708 492 bp mRNA linear EST 03-JUL-2001
DEFINITION IPL 55_H11_b1_A002 Immature panicle 1 (IPL) Sorghum bicolor cDNA,
mRNA sequence.
ACCESSION B1141708
VERSION B1141708.1 GI:14594151
KEYWORDS EST.
SOURCE sorghum.
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
REFERENCE 1 (bases 1 to 492)
AUTHORS Klein,R.R., Cordonnier-Pratt,M.-M., Gingle,A., Sudman,M. and Pratt
,L.H.
TITLE An EST database from Sorghum: developing preanthesis panicles
JOURNAL Unpublished (2001)
COMMENT Contact: Cordonnier-Pratt MM
Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
Email: mmp@arches.uga.edu
Sequences have been trimmed to exclude polyA, vector and regions
below Phred quality 16. The threshold for high quality sequence is
20. Three-prime sequences, which are obtained with PolyMix or T7
Seq primer: JEN REV
High quality sequence stop: 458
POLYA-No.

FEATURES
Source Location/Qualifiers
1..492
/organism="Sorghum bicolor"
/cultivar="Brx623"

/db_xref="taxon:4558"
/clone_lib="Immature panicle 1 (IPL)"
/note="Organ: Developing preanthesis panicles; Vector:
pBluescript II SK(-) from Lambda Zap II; Site 1: XhoI;
Site 2: EcoRI; The library was made from poly-A RNA in the
cloning vector Lambda Zap II. Clones to be sequenced were
prepared by mass excision."
BASE COUNT 115 a 125 c 154 g 98 t
ORIGIN

Query Match 83.9%; Score 343.8; DB 10; Length 492;
Best Local Similarity 91.7%; Pred. No. 4e-69;
Matches 363; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 12 ggcgtcatgaggcagaaacctgcccctcaacattgcaagaagggtcccatctctgtg 71
DB 97 GCGGTATGGGCGAGAACCTTGGCCCTCAACATTGCAGAGAAAGGCTTCCCATCTCTGTC 156
QY 72 tacaacagagcaaacctccaaggtgacagaccgtgacgctgccaagagcaagaac 131
DB 157 TACAACAGGACAACTCCACAGGTTGATGAGACCGTGACGCGGCAAGGCAAGAGAAAC 216
QY 132 ctcccgctcaagcgttcacatgaccgcgcgtcccttggaagtccattcagaaccacgg 191
DB 217 CTTCCTGTGTACGGCTTCCATGACCTCTGATCTTTGTGAACCTCCATTCAAGAACCGCGT 276
QY 192 gtgtgatacatgctcgtcaagccgcgcgcagttgaccacatcgagagctgcga 251
DB 277 GTTGTCATCATGCTTGTCAAGCGTGCGTGCACACAGTTGACACACATTGGCAGCTCGCA 336
QY 252 gctcaactgagagcagggcgactgcatcgtatgagggaagagtgtagcaagaacag 311
DB 337 GCTCATTGGAGCAGAGGCTGACTGTATGATGAGAGGAATGAGTGTATGAGAACACT 396
QY 312 gagaagagagaaagccatggaagagcgcgcctnctgtatcttgcatggtgtctct 371
DB 397 GAGAGGAGGAGAGAGCCATGAGAGAGCGTGGCTCCTCTATCTTGGAAATGGGCGTCTCT 456
QY 372 ggaagaaagagggtgcccgaagagccgctccttgatg 407
DB 457 GGAGGAGAGAGGAGGTCGCCGACAGCAACCTTGTGATG 492

RESULT 3
LOCUS BF267183 531 bp mRNA linear EST 23-OCT-2001
DEFINITION HV_CEA0017D02f Hordeum vulgare seedling green leaf EST library
HVCDNA0004 (Blumeria challenged) Hordeum vulgare cDNA clone
HV_CEA0017D02f, mRNA sequence.
ACCESSION BF267183
VERSION BF267183.2 GI:13263227
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
REFERENCE 1 (bases 1 to 531)
AUTHORS Wing,R., Close,T.J., Kleinbols,A., Wise,R., Wei,F., Begum,D.,
Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi
D.W., Rendon,R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected incompatible (Mia13)
seedling leaf cDNA library
Unpublished (2001)
On Nov 17, 2000 this sequence version replaced gi:11198178.
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293

Email: rwing@clmson.edu
Total hg bases = 427

Seq primer: AATTAACTCCTACTAAAGG
High quality sequence stop: 521.

FEATURES

source

1. 531

/organism="Hordeum vulgare"

/cultivar="C16155 (M1a13)"

/db_xref="taxon:4513"

/clone="HV_CEA0017D02f"

/clone.lib="Hordeum vulgare seedling green leaf EST"

/library="HVCNDA0004 (Blumeria challenged)"

/tissue_type="seedling green leaf"

/lab_host="TUC121"

/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI; C.I. 16155 (M1a13) plants were greenhouse grown in the R wise lab at Iowa State University, Ames, IA; 7 day old green seedlings were challenged with isolate A27 (Ayrmla13) of Blumeria graminis f. sp. hordei, and leaves were harvested 20 and 24 hr post-inoculation and snap frozen; uninoculated leaves were harvested 20 hr post-inoculation (Wei, Wise). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool. Equal quantities of all three RNA pools were combined. poly(A) RNA was purified from the mixture, one cDNA library was made, and 1 million ptu were in vivo excised to give Bluescript SK(-) cDNA phagemids (Choi, Close). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Slimmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhouse A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/g9pages/g9n/31/cover.html)"

BASE COUNT

121 a 148 c 156 g 106 t

ORIGIN

Query Match

Best Local Similarity 79.0%; Score 323.8; DB 10; Length 531;
Matches 352; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

11 cgcgcatcgtgagcagaacctgacctcaacatctgacagagaaggttcccatctgt 70
|||||
75 CGCGCATGCGGCGAGAACCTTCCTCAACATTGCAGAGAAAGCGTCCCATCTCTGT 134
71 gtacaacaggaacacctccaaggtgacagacgctgacagtgacagagaagaa 130
|||||
135 CTACACACAGACACATCAAGGTCGACGAGACCGTCCACGCGCAAGCTAAGAGAAA 194
131 ccttcgcgtctacaggttccatgacccgcgtccttctgaaagtcattcagaagccag 190
|||||
195 CTTTCTCTCTACGCTTTCATGACCTGATCTTTGTCACTTCATTCATGAGGCCACG 254
191 ggtgtgatcatgctcgtcaagcgcgcgcgcagcttgacacacacatcgacgcctgc 250
|||||
255 TGTGCGTCATCATGCTTGTCAAGCGCGTGTCTCGGTTGACACACATCGCCACGCTCGC 314
251 agctcaacttgagacagagcgacgtcatcatcgatggggaggaacagtgatgagaacac 310
|||||
315 AGCACACCTGAGACAGGCGACATGCTGTTGACGAGAGAAAGAGTGTATGAGAACAC 374
311 ggaag 370
|||||
375 AGAAG 434

QY 371 tggagagaagagaggtgcccgaacagggcccgcttcctgatatg 410
|||||
DB 435 TGGAG 474

RESULT 4

AV939826

LOCUS

AV939826

590 bp mRNA

linear

EST 18-JAN-2002

heading stage top three leaves Hordeum vulgare subsp. spontaneum

cDNA clone ba124c17 5', mRNA sequence.

AV939826

GI:18235623

VERSION

AV939826

1 GI:18235623

EST

Hordeum vulgare subsp. spontaneum

Hordeum vulgare subsp. spontaneum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae

Triticaceae; Hordeum.

Sato, K., Saito, D. and Takeda, K.

SOURCE

Hordeum vulgare subsp. spontaneum

Hordeum vulgare subsp. spontaneum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae

Triticaceae; Hordeum.

Sato, K., Saito, D. and Takeda, K.

Barley EST sequencing project in NIG and Okayama Univ

Unpublished (2002)

Contact: Tadashi Shin-I

REFERENCE

1 (bases 1 to 590)

Sato, K., Saito, D. and Takeda, K.

Barley EST sequencing project in NIG and Okayama Univ

Unpublished (2002)

Contact: Tadashi Shin-I

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

AUTHORS

Sato, K., Saito, D. and Takeda, K.

Barley EST sequencing project in NIG and Okayama Univ

Unpublished (2002)

Contact: Tadashi Shin-I

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

JOURNAL

Unpublished (2002)

Contact: Tadashi Shin-I

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshin@genes.nig.ac.jp.

FEATURES

source

1. 590

/organism="Hordeum vulgare subsp. spontaneum"

/strain="H602"

/db_xref="taxon:77009"

/clone="ba124c17"

/clone.lib="K. Sato unpublished cDNA library, strain H602 adult, heading stage top three leaves"

/tissue_type="top three leaves"

BASE COUNT

130 a 167 c 178 g 114 t

/dev_stage="adult, heading stage"

1 others

ORIGIN

Query Match 79.0%; Score 323.8; DB 9; Length 590;
Best Local Similarity 88.0%; Pred. No. 1.7e-64;
Matches 352; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

11 cgcgcatcgtgagcagaacctgacctcaacatctgacagagaaggttcccatctgt 70
|||||
69 CGCGCATGCGGCGAGAACCTTCCTCAACATTGCAGAGAAAGCGTCCCATCTCTGT 128
71 gtacaacaggaacacctccaaggtgacagacgctgacagtgacagagaagaa 130
|||||
129 CTACACACAGACACATCAAGGTCGACGAGACCGTCCACGCGCAAGCTAAGAGAAA 188
131 ccttcgcgtctacaggttccatgacccgcgtccttctgaaagtcattcagaagccag 190
|||||
189 CTTTCTCTCTACGCTTTCATGACCTGATCTTTGTCACTTCATTCATGAGGCCACG 248
191 ggtgtgatcatgctcgtcaagcgcgcgcgcagcttgacacacacatcgacgcctgc 250
|||||
249 TGTGCGTCATCATGCTTGTCAAGCGCGTGTCTCGGTTGACACACATCGCCACGCTCGC 308
251 agctcaacttgagacagagcgacgtcatcatcgatggggaggaacagtgatgagaacac 310
|||||
309 AGCACACCTGAGACAGGCGACATGCTGTTGACGAGAGAAAGAGTGTATGAGAACAC 368
311 ggaag 370
|||||
369 AGAAG 428

Oy	371	tggaggaaggaggtgcccgaacagcccttcattgatg	410
Dd	429	tggaggaaggaggtgcgcccatgccccctcattgatg	468
RESULT	5		
AL504224			
LOCUS			
DEFINITION	AL504224	612 bp	mRNA
ACCESSION	AL504224	Hordeum vulgare Barke roots	linear EST 04-JAN-2001
VERSION	HMO4J10v 5'	Hordeum vulgare	cDNA clone
KEYWORDS	AL504224.1	GI:12030439	
SOURCE	EST.		
ORGANISM	Barley.		
	Hordeum vulgare		
	Eukaryota; Viridiplantae;		
	Spermatophyta; Magnoliophyta;		
	Liliopsida; Poales; Poaceae; Pooideae		
	; Triticeae; Hordeum.		
	1 (bases 1 to 612)		
REFERENCE	Michael, W., Weschke, W., Pleissner, K.-P. and Graner, A.		
AUTHORS	EST sequencing and analysis in barley		
TITLE	Unpublished (2000)		
JOURNAL	Contact: Michalek W		
COMMENT			

FEATURES	Location/Qualifiers
source	1. .612

BASE COUNT	ORIGIN	ampligates.	the maximum length was set to 700 bp
140 a	166 c	177 g	126 t
			3 others

Query Match	79.0%	Score 323.8;	DB 9;	Length 612;
Best Local Similarity	88.0%;	Pred. No. 1.7e-64;		
Matches 352; Conservative	0;	Mismatches 48;	Indels 0;	Gaps 0;

Accession	Sequence	Position
QY	11 cgcagctctggagcgagaaaccttgcaccttaacaatctgcagagaagaagggtctcccatctctgt	70
Db	47 CGCGTCATGGGGCGAAGAACCTTGGCCCTCAAAATTGSCAAGAAAGGCTTCCCATCTCTGT	106
QY	71 gtacacacggcgacaaactccaagcttgagacgagacccgtgcaagctgycgaagacagaaagaaa	130
Db	107 CTACACACGGACGCAATCTCAAGTGTGAGAGAAACCGTCACGCGCCCAAGCTATGAAGGAAA	166
QY	131 ccttcacgctctaaagcttccaagaccgcgctccctcttgtgaagtcacatccgaagccacg	190
Db	167 CCTTCTCTCTACGGATTTCATGACCCCTGCACTCCTTTGTCAACATCCATTCGAAAGCCACG	226
QY	191 ggtggatcatctgtctgtcaagcgcgcgcgacgatttgaccacagacacatcgagacgctcgc	250
Db	227 TGTGTGATCATCTGCTGTGTCAAGCGCGGNGCTCCGGTTGACACAGACATCCGCAAGCTTCG	286
QY	251 agctcactctggaagcagcgacatcatcatcgtatgggggggaacgagctggtcatcagaacac	310

Accession	Sequence	Position
Db	AGCACACTGGAGGAGGCGCCACTGCATCTTTGACGAGGAAACAGTGTGATAGAAAC	346
Oy	ggagaagagaggaagaagcgcattgagagagagcgccgctctcgtatctgcaatggggtctc	370
Db	AGAAAGGAGGAGGAGAGGCGATGCGAGGAGCGCTGGCACTCTTCACTTCGGTATGGGTGTTTC	406
Oy	tgagaggaagaggggtgcgccgcaacggcccgctctctgatg	410
Db	TGGAGAGGAGGAGGATGCCGCCCTATGGCCCGTCCATCATATG	446

RESULT	6
LOCUS	BE216705
DEFINITION	BE216705 HV_CEB00111E16f Hordeum vulgare seedling green leaf EST library HV_CEB00111I16f, mRNA sequence.
ACCESSION	BE216705
VERSION	BE216705.2
KEYWORDS	EST. barley.
SOURCE	Hordeum vulgare
ORGANISM	

REFERENCE
AUTHORS
Wing, R., Close, T. J., Kleinholz, A., Wise, R., Wei, F., Bequm, D.,
1 (bases 1 to 722).
; Trillaceae; Hordeum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
1 (bases 1 to 722).

TITLE
JOURNAL
COMMENT

W., Fenton, R.D., Oates, R. and Main, D.
Development of a genetically anchored EST resource
for barley genomics: Blumeria Infected Incompatible (MIae) seedling
leaf cDNA library
Unpublished (2001)
On Jul 3, 2000 this sequence version replaced gl:8904317.

Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwinge@clemson.edu
 Total bp bases = 459
 Seq primer: AATTACCTCCTACTAAGG
 High quality sequence stop: 617.
 Location/Qualifiers
 1..722
 source

```

/organism="Hordeum vulgare"
/cultivar="C116151 (M1a6)"
/db_xref="taxon:4513"
/clone="HV_CED0011E16f"
/clone_id="Hordeum vulgare seedling green leaf EST
library HVCDNA0005 (Blumeria challenged)"
/tissue_type="seedling green leaf"
/lab_host="SOLR"
/notes="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
C.I. 16151 (M1a6) plants were greenhouse grown in the R
Wise lab at Iowa State University, Ames, IA; 7 day old
green seedlings were challenged with isolate 5874 (AvrM1a6
) of Blumeria graminis f. sp. hordei, and leaves were
harvested 20 and 24 hr post-inoculation and snap frozen;
uninoculated leaves were harvested 20 hr post-inoculation
(Wel, Wise). In the TV Close lab at the University of
California, Riverside, total RNA was prepared from each
sample pool, equal quantities of all three RNA pools were
combined, poly(A) RNA was purified from the mixture, one
primary unamplified cDNA library was made, and 1 million
pfu were in vivo excised to give pluscript SK(-) cDNA
phagemids (Choi, Close). Phagemids were plated and picked
at the Clemson University Genomics Institute (CUGI) (Begum
, Palmer, Fritsch, Atkins and Wang). Plasmid DNA
preparations, DNA sequencing and sequence analysis were
performed at CUGI (Wing, Yu, Fritsch, Henry, Simmons, Oates
, Rambo, Malin). The sequence has been trimmed to remove

```

vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wang R, Kleinoffs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/ggpages/bqng/31/cover.html>)"

Query Match	79.0%;	Score 323.8;	DB 9;	Length 722;
Best Local Similarity	88.0%;	Pred. No. 1.8e-64;		
Matches 352; Conservative	0;	Mismatches 48;	Indels 0;	Gaps 0

QY	11	cgcgccatgaggagaaaccttgcctccaacatgtgagagaagaggtcttcccactctgt	70
Db	51	CGCGGTATGTGGGCGAGAACTTGCCTCTCAACATTGCAGAAAGAGCTTCCCATCTCTGT	110
QY	71	gtacaacagagacaacccctccaagtgacgagaaacccgtgcaagctgccaagycagaagaa	130
Db	111	CTACACAGAGGACGACATTCGAAGTTCGACGAGACCGCTCCACGGCCCAAGCTAGAGGAA	170
QY	131	ccctcccgctcagcgcttccatgaccccgcgctccctgttgaagtcacatcagaagccag	190
Db	171	CCTTCCTCTCAACGGTTTCATGACCTCGATCCTCTTGTCAACTCCATTCAGAAAGCCACG	230
QY	191	ggtgtgatacatgtctgccaagcgcgcgccagcttgaccagaacacatcgcgagctcgc	250
Db	231	TGTGCTATCTATGCTTTGTCAAGCGCGGTGTCTCGGTGACCAACCTCCACCGCTCGC	290
QY	251	agctcaacttggacgaaggcgactgcatcatalgcgatggggagaaacagatggtacagaacac	310
Db	291	AGCACAACCTGGAGAGGCGCAGCTCATCTGTTGACGGAGGAACGAGTGTATGAAACAC	350
QY	311	ggagagagaggaagaagccatgtgagagagcgcgccctmcctlatcttgcacttggcattgctc	370
Db	351	AGAAAGGAGGAGAGGCGATGAGGAGCGGCGACTCTCTTACTCTCGTATGGGTGTTTC	410
QY	371	tgagagaaagaggtgcccgcacagccccgttctctatg	410
Db	411	TGGAGGAGAGGAGGTGGCCGCCATGGCGCCGTCCATATG	450

RESULT				7
LOCUS	BEA13061			
DEFINITION	BEA13061	886 bp	mRNA	linear EST 24-JUL-2000
ACCESSION	MCG015.E05R990625	ITEC MCG Barley Leaf/Culm Library	Hordeum vulgare	
VERSION	CDNA clone MCG015.E05,	mRNA sequence.		
KEYWORDS	BEA13061			
SOURCE	BEA13061.1	GI:9410907		
ORGANISM	EST.			
	Barley.			
	Hordeum vulgare			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae			
	; Triticeae; Hordeum.			
REFERENCE	1 (bases 1 to 886)			
AUTHORS	Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P., Hermann,R.G., Holton,T., Jacquemin,I.M., Jia,J., Jouderier,P., Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y., Peccoloni,N., Quiset,C., Schuch,W., Selvaraj,G., Shariflou,M., Sorrells,M., Waburton,M. and Weizel,G.			
TITLE	International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae Unpublished (2000)			
JOURNAL COMMENT	Contact: Graner A Institute for Plant Genetics & Crop Plant Research Corrensstr. 3, D-06466 Gatersleben GERMANY Tel.: 49 39482 5521			

Fax: 49 39482 5137
Email: a_graner@ipk-gatersleben.de
International Triflicaceae EST Cooperative (ITEC)
<http://wheat.pw.usda.gov/gsnome>
teat.1@ipk-gatersleben.de

BASE COUNT	202 a	224 c	258 g	186 t	16 others
ORIGIN					

Query Match	Best Local Similarity	79.0%;	Score 323.8;	DB 10;	Length 886;
Matches	352;	Conservative	0;	Mismatches	48;
				Indels	0;
				Gaps	0;
OY	11	cgcggtcatggcgacgaaccttgccttcaacatctgcagagaaaggttcccatctctgt	70		
Db	47	CGCGGTCTCATGGGGGCGAGAACTTGGCCCTCAACATTCGACAGAAAGGCTTCCCATCTTCTGT	106		
OY	71	gtacaacggagcaacactccaaggctgagagaaacgctgagacgttgcgcaagagcaagagaa	130		
Db	107	CTACACACGAGCAGCATCCAAAGTGTGACGAGACCGTCCAGCGCCGCAAGCTTGAAAGGAAA	166		
OY	131	ccttcgccttcaagcttccatctgacacccgcgcttcttltgaagtlcatctagaagccagc	190		
Db	167	CCTTCCTCTCAAGGTTTCCATGACCCGTGCAATCTCTTGTCAACCTCATTCAGAAACCAAG	226		
OY	191	ggtgtgtcatcatgcttcgtcaaggccgcgcgcgaattgaccagacatcgcgaagctgc	250		
Db	227	TGTGCTCTCATAGCTTGTCGAAGCCGGGTCTCCGGTTTACACAGACCATTCGCCACTCTGC	286		
OY	251	agctcaacttggagcagcgagactgcatactcgatbtggggagcaagatgtgttcacgaacac	310		
Db	287	AGCACACTTGAGCAGCGGCGACTGCATCGTTGACGAGAAACGAGTGTATGAAACAC	346		
OY	311	ggaagagagagaaagccatctgagagagcgcgctnctgtatcttgcgcatgggtgtctc	370		
Db	347	AGAAAGGAGGAGAAAGCGATGAGAGACGTCGACTCTTACCTCCGTATGGGTGTTC	406		
OY	371	tggagagaaagaggtgtccgcgaagcgccgttcttactgt	410		
Db	407	TGGAGAGAGAGGGGTGCCCGCATAGGCGCCGCTCATGATG	446		

RESULT	8
LOCUS	BM370860
DEFINITION	445 bp mRNA linear EST 10-JAN-2002 EBro04_S0002_J06_R IGF barley Ebro04 library Hordeum vulgare cDNA
ACCESSION	BM370860
VERSION	BM370860.1
KEYWORDS	GI:18114250
SOURCE	EST.
ORGANISM	barley.
REFERENCE	Hordeum vulgare
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidaeae ; Triticeae; Hordeum. 1 (bases 1 to 445) Headley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardle, L., Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R. Development of Barley Transcriptome Resources Unpublished (2001) Contact: Waugh R Unit of Genomics Scottish Crop Research Institute Invergowrie, Dundee, DD2 5DA, Scotland, UK Tel: 00 44 1382 562731 Fax: 00 44 1382 562426
TITLE	
JOURNAL	
COMMENT	

Db 182 GTCATCATGCTTTGTCAAGGCGGTCTCCGGTTGACCAAGACATATGCCACAGCTGCACAGA 241

QY 255 cacttggagacagagcgactgcactgcatactcgaatggggggaacagatggtacagaaacagag 314

Db 242 CACCTGGAGCAGGGCGACGATGCATCTTTAGCAGGAGAAACGATGGTATGACACACAGAA 301

QY 315 aggaagggaagagccatctggagagagcgccctnctgtatcttggatagtggtgtcctctga 374

Db 302 AGGAGGGGAAAGCCATGGAGAGGAGTGTGACTCCTCACTCCGATATGGGTGTTTCTTGA 361

QY 375 ggaagagaggttgcgcgaacgagcccgctcttga 410

Db 362 GGAGAGAGAGGTCCCGCCCATAGGCCCGTCCATGATG 397

RESULT	10
BE471136	
LOCUS	
DEFINITION	BE471136 466 bp mRNA linear EST 28-JUL-2000
ACCESSION	WHE0284_C07.E14S wheat drought-stressed seedling cDNA library
	Triticum aestivum cDNA clone WHE0284_C07.E14, mRNA sequence.
	BE471136

ACCESSION	BE471130
VERSION	BE471136.1
KEYWORDS	GI:9561627
SOURCE	EST.
ORGANISM	bread wheat.
	Triticum aestivum

REFERENCE
AUTHORS
Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han
I (bases 1 to 466)
Triticaceae, Triticum.
Euaristota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
Triticaceae, Triticum.

TITLE The structure and function of the expressed portion of the wheat genomes - Drought-stressed seedling cDNA library

JOURNAL Unpublished (2000)

COMMENT Contact: Olin Anderson

US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: coandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: StrataGene SK primer.

FEATURES	Location/Qualifiers
source	1. .466

```

/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE0284.C07.E14"
/clone_1b="wheat drought-stressed seedling cdna library"
/tissue_type="Seedling without endosperm"
/dev_stage="Five day old seedling"

```

/lab_host="E. coli SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid:
Site_1: EcoRI; Site_2: XhoI; Seeds were surface-sterilized,
germinated and grown aseptically in the dark at room
temperature on filter paper with water, nystatin and
cefotaxime in covered crystallization dishes. Five-day old
seedlings were incubated for one day at 90° RH. After
removing endosperm, seedlings were transferred to
desiccator jar containing saturated MgSO₄ at room
temperature for 24 hr. The tissue, total RNA, and poly(A)
RNA were prepared, a cDNA library was made, and the cDNA
clones were in vivo excised to give Bluescript phagemids
in the TJ Close lab (Choi, Close, Fenton) at the
University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."

BASE COUNT	106	134	135	91
ORIGIN	A	C	G	T

Query Match	78.28;	Score 320.6;	DB 10;	Length 466;
Best Local Similarity	87.58;	Pred. No. 8.3e-64;		
Matches 350;	Conservative 0;	Mismatches 50;	Indels 0;	Gaps 0;

OY	11	cgcggttcattgtaggcagaacctgtgccttcacacattgcagaagaaggtgttcccatctcgt	70
Db	49	cgccgcgcataggccacgaamaacttgccttcacacattgcagaagaaggtgttcccatctcgt	108
OY	71	gtacacacaggaacaacctccaaggttgagcagaagacctgcagcgtgtccagaagcgccagaagaa	130
Db	109	ctacacacaggaacacctccaaggttgagcagaagacctgcagcgtgtccagaagcgccagaagaa	168
OY	131	ccttcgcgctcctacagcgttccttcacagcccgcgcttccttggaaatccattcagaagccag	190
Db	169	ccttctctctctacagcgttccttcacagcccgcgcttccttggaaatccattcagaagccag	228
OY	191	ggtgtgtacatcgtctcgttcgaagcgcgcgccaaagtgtgacagacatccgcgaactgcg	250
Db	229	tgtctgtcatcatcagctgtgttcaaggccgggtctcctgttgaccagaccatccgaacgcgtcc	288
OY	251	agctcaacttgagagcagcgagactgcatactgatatggagggaaccgagtgttaagaagaac	310
Db	289	acacacacctggagccagggcgactgcactcgttgatggagagaaacgaatgtaacagacacac	348
OY	311	ggagaggaaggaaggaagccaattgagagagcgcgactnctgtatctctgagatggtgtctc	370
Db	349	ggaaaggagaggaaggaagcgatggagagagcggtgagactctctacactcgggatgggtgttc	408
OY	371	tggaggaagaaggaaggtgtcccgcaagcgccgcctccttgatg	410
Db	409	cggagagagagaggtgtcccgcaagcgccgcctcctccttgatg	448

RESULT 1.1
B1543081

LOCUS B1543081 531 bp mRNA linear EST 04-SEP-2001
DEFINITION 949072H04.y1 949 - Juvenile leaf and shoot cDNA from Steve Moose
Zea mays cDNA, mRNA sequence.

ACCESSION	B1543081
VERSION	B1543081.1
KEYWORDS	GI:15427259
SOURCE	EST.
	Zea mays.

ORGANISM *Zea mays*
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; *Zea*.

REFERENCE	1 (bases 1 to 531)
AUTHORS	Walbot,V.
TITLE	Maize ESTs from various cDNA libraries sequenced at Stanford University

JOURNAL
COMMENT
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences

Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: wai@cs.stanford.edu
Plate: 949072, row: H, column: 04.

FEATURES	location/qualifiers
source	1. .531

/organism="Zea mays"
/cultivar="W64A"
/db_xref="taxon:4577"
/clone_id="949 - juvenile leaf and shoot cDNA from Steve

```

Moose"
/tissue_type="Immature leaf primordium and vegetative
meristem"
/dev stage="4 stages from 3-13 days after imbibing"

```

```

/ab_host="E. coli X100"
/ote="Organ: juvenile vegetative shoots; Vector:
pAD-GAL4-2.1; Site_1: EcORI; Site_2: XhoI; Equal amounts

```

of total RNA by weight from 4 tissue sources (see below) were pooled, polyA⁺ RNA isolated, and cDNA synthesized for EcoRI (5') and XhoI (3') directional cloning into lambda HybriZap vector from Stratagene. Tissue Sources: 1. Whole shoots 3 days after sowing/imbibing in wet soil. 2. Basal 1.5 cm shoots 6 days after sowing - includes yellow portions of developing leaves 1-5, primordia from 6-8, and the vegetative apex. 3. Non-green portions of developing leaves 4-5 and the vegetative apex, including adult leaf primordia, 9 days after sowing. 4. Partially expanded and green leaves 4-5 at 13 days after sowing."

BASE COUNT 105 a 156 c 173 g 97 t

ORIGIN

Query Match 77.8%; Score 319; DB 10; Length 531;

Best Local Similarity 87.2%; Pred. No. 2e-63;

Matches 349; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 11 cgcggtcatgggagcaaaccttgcctcaacattgcagagaagaggtcccatctctgt 70
 Db 103 CGCGGTCTATGGACAGAACTTGCCTCAACATCGCGGAGAAAGGTTCCCTATCTCGGT 162
 QY 71 gtacacagagcaacctccaaggtgagagaccgttgagagctgcacagagaagaa 130
 Db 163 CTACACAGAGACGACCTCCAGGTTGATGAGACGTCGACGCTCCAGAGTCAAGGAA 222
 QY 131 ccttcgcgtacagcttcacatgcacccgcgtccttcttgagatccattcagagccag 190
 Db 223 CTTCCCGCTGTGGTTTCCAGACCCGCGCTCTGTGAGCTCCATCCAGAACCCCG 282
 QY 191 ggttgatcatgtctgtcaagcgcgccagttgcacagacatcgagcgtctgc 250
 Db 283 TGTGTCATCTATGCTCGTCAAGGCTGGGCGCGGTGACACAGACCATTTGCGACGCTGCG 342
 QY 251 agctcaacttgagagcagcgactcatcatcgtatgagggagagagtgtagaagaaac 310
 Db 343 GGGCAGACTTATGAGGGGAGCTGTATGCTGATGTCGACAGAGTGTGAGAACAC 402
 QY 311 ggaagagagagagagagcattgagagagcgcgccctctgtatcttgagcatgggtctc 370
 Db 403 GGAAGAGAGCGAGAAAGCGATGAGAGAGCGGGGCTCTTATCTTATGTCATGGCGCTCTC 462
 QY 371 tggaggaagagaggtgcccgaacgagccgctcttgatg 410
 Db 463 CGGAGGAGAGGAGGCTGCCCGCATGCGCCCTGATG 502

RESULT 12

BE493869

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BE493869 547 bp mRNA linear EST 02-AUG-2000
 WHE1276_F08_K16Z Secale cereale anther cDNA library Secale cereale
 BE493869 BE493869
 BE493869.1 GI:9660462
 EST.
 rye.
 Secale cereale
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 1 (bases 1 to 547)
 Anderson, O.D., Butler, E., Chao, S., Choi, D.W., Close, T.J., Fenton
 R.D., Gustafson, J.P., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R.,
 Miller, R., Rausch, C.J., Ross, K., Seaton, C.L. and Tong, J.C.
 The structure and function of the expressed portion of the wheat
 genomes - Another cDNA library from rye
 Unpublished (2000)
 Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105959773

Fax: 5105959818
 Email: oanderson@w.usda.gov
 Sequence have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20
 Seq primer: Stratagene SK primer.
 Location/Qualifiers
 1. 547
 /organism="Secale cereale"
 /cultivar="Blanco"
 /db_xref="taxon:4550"
 /clone="WHE1276_F08_K16"
 /clone_1ib="Secale cereale anther cDNA library"
 /tissue_type="Anther"
 /dev_stage="Adult plant before anthesis"
 /lab_host="E. coli SOUT"
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
 site_1: EcoRI; site_2: XhoI; Plants were grown in the
 greenhouse. Anthers were harvested and pooled from early
 meiosis to late meiosis. The tissue, total RNA, and
 poly(A) RNA were prepared (Butler, Ross and Gustafson) at
 University of Missouri, Columbia. A cDNA library was
 made, and the cDNA clones were in vivo excised to give
 phagescript phagemids in the TJ Close lab (Choi, Close,
 Fenton) at the University of California, Riverside.
 Plasmid DNA preparations and DNA sequencing were performed
 in the OD Anderson lab (all other authors)."

BASE COUNT 121 a 149 c 160 g 117 t

ORIGIN

Query Match 77.8%; Score 319; DB 10; Length 547;

Best Local Similarity 87.2%; Pred. No. 2.1e-63;

Matches 349; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 11 cgcggtcatgggagcaaaccttgcctcaacattgcagagaagaggtcccatctctgt 70
 Db 48 CGCGGTCTATGGGAGAGAACTTGCCTCAACATTTGCCGAGAAAGGCTTCCCATCTCTGT 107
 QY 71 gtacacagagcaacctccaaggtgagagaccgttgagagctgcacagagaagaa 130
 Db 108 CTACACAGAGACGACCTCCAGGTTGATGAGACGTCGACGCTCCAGAGTCAAGGAA 167
 QY 131 ccttcgcgtacagcttcacatgcacccgcgtccttcttgagatccattcagagccag 190
 Db 168 CTTCCCGCTGTGGTTTCCAGACCCGCGCTCTGTGAGCTCCATCCAGAACCCCG 227
 QY 191 ggttgatcatgtctgtcaagcgcgccagttgcacagacatcgagcgtctgc 250
 Db 228 CTTCCCGCTGTGGTTTCCAGACCCGCGCTCTGTGAGCTCCATCCAGAACCCCG 287
 QY 251 agctcaacttgagagcagcgactcatcatcgtatgagggagagagtgtagaagaaac 310
 Db 288 TGCACACCTGAGAGCAAGGTGACTGCTGTGATGAGAGAAAGTGTGAGAACAC 347
 QY 311 ggaagagagagagagcattgagagagcgcgccctctgtatcttgagcatgggtctc 370
 Db 348 GGAAGAGAGCGAGAAAGCGATGAGAGAGCGGGGCTCTTATCTTATGTCATGGCGCTCTC 407
 QY 371 tggaggaagagaggtgcccgaacgagccgctcttgatg 410
 Db 408 CGGAGGAGAGGAGGCGGCCCGCATGCGCCCTGATG 447

RESULT 13

AM448282

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AM448282 823 bp mRNA linear EST 03-JAN-2001
 BRY 1785 BRY Trilicium aestivum cDNA clone P61-10, mRNA sequence.
 AM448282 AM448282
 AM448282.1 GI:12018817
 EST.
 bread wheat.
 Trilicium aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
AUTHORS	Triticaceae; Triticum.
TITLE	1 (bases 1 to 823)
JOURNAL	Clarke/B.C., Hobbs/M. and Appels/R.
COMMENT	Genes active in developing wheat endosperm Unpublished (2000) Contact: Bryan Clarke Division of Plant Industry C.S.I.R.O. GPO Box 1600, Canberra, ACT, Australia Tel: 61 2 6246 5054 Fax: 61 2 6246 5000 Email: bryan@pl.csiro.au
FEATURES	Location/Qualifiers
source	1. 823
	/organism="Triticum aestivum"
	/cultivar="Wyna"
	/db_xref="taxon:4565"
	/clone="p61-10"
	/clone_1lb="BRY"
	/cell_type="endosperm"
BASE COUNT	180 a 233 c 247 g 163 t
ORIGIN	

Query Match	77.8%	Score 319	DB 93	Length 823
Best Local Similarity	87.2%	Pred. No. 2.4e-63		
Matches 349	Conservative 0	Mismatches 51	Indels 0	Gaps 0

OY	11	cgcggtcatgggaggaacattgcctccaacatctgacgagaagaggtctcccatctctgt	70
Db	153	GGCGGTATGGGGGAGAACTTGGCCCTCMACTTGGCGAGAAAGCTTCCCATCTCCGT	212
OY	71	gtacaacagagcaaacctccaagttgacgagccgtgcagctgtgccaaagcagaagynaa	130
Db	213	CTACAAACAGGACCCACTCTCAAGTGCATGAGACCGTTACACGGCGCCCAAGCTAGAGGAA	272
OY	131	cccttcogtctaaggcttccatctgaccccggtcctttgtgaagtccatcttaagaagccag	190
Db	273	CGTTCTCTCTCAAGCGTTCATGACCCCTGATCTCTTGTCMACTCCATCAGAAGCCACG	332
OY	191	ggtgtgtacatgtctgtcctcaagcgcggcgcgaattgacacacatctgcgcgcctcgc	250
Db	333	TGTGCTATCATGCTTGTTCAAAGCCGGCGCTCCGGTTGACACAGACTATTCGCCACGCTCGC	392
OY	251	agctcaacttggagcagagggcgactgcatactcgtatgaggggagacagagtgcgtacagaaac	310
Db	393	AGCACACCTGGACGAGGGTGACTCATTCTGTTGAGGAGAAACGAGTGTATCGAGAAAC	452
OY	311	ggagagagagagagaagccatgtgagagacgcgcgcttmcgtatcttgcattggatgggtctc	370
Db	453	GGAAGAAGGAGAGAGGCGATGAGAGAGCGAGCTCTCTACCTCGAGTGGGTGTTTC	512
OY	371	tggaggaagagaggtgtccgcgaacgcgcctctcttgatg	410
Db	513	CGAGAGAGAGGAGGTGCCCGCCATGGCCCTCCCTCATATG	552

RESULT	14
LOCUS	Bf630844
DEFINITION	Bf630844 875 bp mRNA linear EST 22-OCT-2001
ACCESSION	U58500.1
VERSION	1
KEYWORDS	
SOURCE	barley.
ORGANISM	Hordeum vulgare Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; ; Triticeae; Hordeum. 1 (bases 1 to 875)
REFERENCE	

AUTHORS Ming-R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Y
 , Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton
 , R.D., Oates,R. and Main,D.
TITLE Development of a genetically and physically anchored EST resource
 for barley genomics: Morex drought-stressed seedling shoot cDNA
 library
JOURNAL Unpublished (2001)
COMMENT On Dec 19, 2000 this sequence version replaced g1:11895002.
CONTACT RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rtwing@clemson.edu
 Total hg bases = 444
 Seq primer: AATTACCCCTCAGTAAGG
 High quality sequence stop: 543.
 Location/Qualifiers
 1..875

FEATURES	Location/Qualifiers
source	1. .875

/note=Vector: lambdaZAP; Site.1: EcoRI; Site.2: XhoI;
 Seeds were surface sterilized then germinated under aseptic
 conditions in the dark at room temperature on filter paper
 with water, nystatin and cefotaxime in covered
 crystallization dishes. Five-day old seedlings were
 incubated at 90% RH for 24 hr. Shoots were then harvested,
 total RNA was prepared, poly(A) RNA was purified, one
 primary unamplified cDNA library was made, 600000 pfu were
 in vivo excised to give phuescript SK(-) cDNA phagemids.
 These steps were performed in the TJ Close laboratory at
 the University of California, Riverside (Choi, Close,
 Penton). Phagemids were plated and picked at the Clemson
 University Genomics Institute (CUGI) (Begum, Palmer,
 Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
 sequencing and sequence analysis were performed at CUGI
 (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
 The sequence has been trimmed to remove vector sequence
 and contains a minimum of 100 bases of phred value 20 or
 above. For more details on library preparation and
 sequence analysis see
<http://www.genome.clemson.edu/projects/barley>. To order
 this clone see <http://www.genome.clemson.edu/orders> Also
 see Close TJ, Wing R, Kleinbotts A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>

Query Match	77.3%	Score 317	DB 10	Length 875
Best Local Similarity	86.8%	Pred. No. 7e-63		
Matches 347	Conservative 0	Mismatches 53	Indels 0	Gaps 0

Qy	11	cgcgcgtacatgggcagaaacctgtccctcaaatcagagaagaagttcccatctctgt	70
Db	143	CGCCGTCATGGGGCGAAGACTTGGCCCTCAACTTCGACAGAAAGGCTTCCCATCTCTGT	202
Qy	71	gtacacacaggaacaacctccaaagcttgagcagagacgctgcagcgtgcacaaggcagaagaaa	130
Db	203	CTACAAACAGGAGCAGCATCCAGATGAGAGGACGCTCAGCGTGCCAAAGCTAAGAGGAAA	262
Qy	131	cccttcgcgtacagagcttcacatgaaccgcgcgtcctcttcttgaaagtcacatcagaagccagc	190
Db	263	CCCTTCCTCTCTCAACGGTTTTCATGACCCGCACTCCCTCTCTCAACTTCATTCATCGAAGCCACG	322

RESULT	15
LOCUS	BI074740
DEFINITION	BI074740 536 bp mRNA
ACCESSION	IP1_15_F05.b1.A002 Immature panicle 1 (IP1) Sorghum bicolor cDNA,
VERSION	BI074740
KEYWORDS	BI074740.1 GI:14513397
SOURCE	EST.
ORGANISM	Sorghum
	Sorghum bicolor

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 536)	Klein, R.R., Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M. and Pratt, L.H.	An EST database from <i>Sorghum</i> : developing preanthesis pannicles	Unpublished (2001)	
	Contact: Cordonnier-Pratt MM			

The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
Email: mmpirat@uga.edu

Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for high quality sequence is 20. Three-prime sequences, which are obtained with PolyTmX or T7 sequencing primer, are presented as the reverse complement.

Seq. primer: JEN REV
High quality sequence stop: 536
PolyA-No.

FEATURES	Location/Qualifiers
source	1. .536

```

/organism="Sorghum bicolor"
/cultivar="BTx623"
/db_xref="taxon:4558"
/clone_lib="Immature panicle 1 (IP1)"
/notes="Organ: Developing preanthesis panicles; Vector:
pBluescript II SK(-) from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; the library was made from poly-A RNA in the
cloning vector lambda Zap II. Clones to be sequenced were
prepared by mass excision."
BASE COUNT
122 a 129 t
138 c 167 g

```

Query Match	77.0%;	Score 315.6;	DB 10;	Length 536;
Best Local Similarity	91.7%;	Pred. No. 1.2e-62;		
Matches 333;	Conservative 0;	Mismatches 30;	Indels 0;	Gaps 0;

DY 12 gcgcgtcattgggacagaaaccttgcctccataacattgcagaaaaagtctcccatctctgtg 71
|||||
|||
Db*, 174 GCGGTCATGGGGGCAGAACCTTGCCCTCAACATTGCAGAAAAGGCTTCCCCTCTCTGTCTC 233

QY	72	tacaaagaacaacctcccaaggttgacagagccgttgaaagcttgcaagagcaagaaggaac	131
Db	234	TACAAAGAACACTCCAAAGTTGATGACCGCTGGCAAGGCAAGAGGAAC	293
QY	132	cttcocgctcaagcgttcacatgaaccccgctcctctgttgaaagtcacatcagaaccacg	191
Db	294	CTTCTGTGTACGGCGTTCCATGACCCGTGACATCTTTGTGAACATCCATTCAAGAGCCGCT	353
QY	192	gtgagatcatcagctccgtcaagagcgcgcgccagttgacagagccatcaggaacgttcga	251
Db	354	GTGTGCATCATGCTTGTCTAAAGGCTGTGTCACCAATTAACAGACCATTTGGACGTTGGCA	413
QY	252	gctcaacttggagcaagggcgacatgcataatcgaatggggggaacagatgttatcgaagaacg	311
Db	414	GCTACTTGGAGCGGGGTGACTGTATCATTTGATGAGGAGGAATGAGTGTGGAACACT	473
QY	312	gaagagaggggaagagcattgaggaagcgcgccctnctgtatcttgcacaggtgctctc	371
Db	474	GAGAGGAGGGGAGAAAGGCGCATGAGAGACGTGGCTCTCTATCTTGGAAATGGGCGCTCT	533
QY	372	gga 374	
Db	534	GGG 536	

Search completed: July 3, 2002, 03:38:46
Job time: 43306 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 3, 2002, 03:38:46 ; Search time 6582.52 Seconds

(without alignments)
469,547 Million cell updates/sec

Title: US-09-300-482-27

Perfect score: 229
1 cagaccattttctcgtc.....ctcaattatgggagacaa 229

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estbta:*
2: em_esthum:*
3: em_estin:*
4: em_estinu:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pin:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	152.2	66.5	566	10	B1972100 sag87c05.
2	139.4	60.9	561	9	BE022117 sm67f12.Y
3	113.4	49.5	532	9	AW719787 LJNEST10A
4	110.4	48.2	430	9	AV406682 AY406682
5	108.6	47.4	630	9	AW695821
6	105	45.9	355	10	BG447744 NF093E04E
7	101	44.1	499	9	BE020243 sm42d04.Y
8	100	43.7	435	10	BE640081 NF027D02I
9	96.2	42.0	573	9	AW586409 EST318032
10	96	41.9	367	10	BF632565 NF032C07D
11	96	41.9	430	9	AL368071 MCB422A07
12	94	41.0	492	10	BI262817 NF091D06E
13	89.6	39.1	420	9	AL382847 MCB10C10
14	88.2	38.5	627	10	BF645919 NF040E03E
15	87.4	38.2	337	9	AL367204 MCB412H03
16	87.4	38.2	344	10	BF636762 NF002H05L
17	87.4	38.2	468	10	BI266601 NF101F03I

18	87.4	38.2	479	9	AL365745
19	87.4	38.2	481	9	AL365743
20	87.4	38.2	485	10	BF639372
21	87.4	38.2	489	10	BI267224 NF099D04I
22	87.4	38.2	533	10	BI264810
23	87.4	38.2	574	10	BF639271 NF030C11I
24	87.4	38.2	630	9	AW688619 NF009P08S
25	87.4	38.2	646	10	BF642248 NF066E08I
26	87.4	38.2	664	10	BI267384 NF103F09I
27	87.4	38.2	677	10	BI308974 EST530384
28	87.4	38.2	684	10	BI266145 NF100H06I
29	85.6	37.4	321	9	AV410206
30	85.6	37.4	379	9	AV410953
31	85.6	37.4	394	9	AV425788
32	85.6	37.4	548	10	BI419927 LJNEST42a
33	85.6	37.4	548	10	BI420937 LJNEST63c
34	82.2	35.9	606	9	AW299197 EST306007
35	81	35.4	559	10	BM093703 sa113b10.
36	81	35.4	614	10	BF066944
37	80.6	35.2	548	9	AL368600
38	80.4	35.1	670	10	BG598747
39	79.6	34.8	520	10	BI920404
40	79.4	34.7	733	9	AI055038
41	79	34.5	379	10	BG239631
42	78.4	34.2	151	10	BF645629 NF030F01E
43	78	34.1	332	9	BE204727
44	78	34.1	504	10	BE450814
45	78	34.1	556	10	BI179863

ALIGNMENTS

RESULT 1
LOCUS B1972100
DEFINITION sag87c05.y1 Gm-cl084 glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-cl084-1257 5' similar to TR:022111 022111 6-PHOSPHOGUADONATE
DEHYDROGENASE ; mRNA sequence.
B1972100.1 GI:16346505

ACCESSION B1972100
VERSION
KEYWORDS
SOURCE
ORGANISM

soybean.
glycine max

REFERENCE 1 (bases 1 to 566)
AUTHORS Shoemaker,R., Kelm,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,
A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wylie,T., Underwood,K., Steptoe,M., Rheising,B., Allen,M., Bowers,
Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,
R., Ritzer,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., Mccann,
R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntville, AL 35801 For further information
call: (800)-533-4363 or contact via email: cut@resgen.com
High quality sequence stop: 421.
Location/Qualifiers
1..566
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl084-1257"

TITLE JOURNAL
COMMENT

FEATURES
source

```

/clone_1lb="Gm-cl084"
/tissue_type="Etiolated hypocotyls (Williams 82)"
/lab_host="DH10B"
/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI. The cDNA library was constructed by M. Bhattacharya
from mRNA isolated from etiolated hypocotyls from the
cultivar Williams 82. Tissue was inoculated with
Phytophthora soyae race 1 and tissues were harvested 2 and
4 hours following infection. The library is the pool of
these two time points. Complementary DNA was synthesized
from mRNA using a primer consisting of a poly(dT) sequence
with a XhoI restriction site. EcoRI adapters were ligated
to the blunt-ended cDNA fragments followed by XhoI
digestion. The cDNA fragments were directionally cloned
into the EcoRI-XhoI restriction site of the pBluescript
vector. The ligated cDNA fragments were transformed into
DH10B host cells (Gibco BRL). This library was constructed
by M. Bhattacharya in the laboratory of Dr. Randy
Shoemaker at Iowa State University."

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BASE COUNT      158 a      107 c      140 g      161 t
ORIGIN

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Query Match      66.5%; Score 152.2; DB 10; Length 566;
Best Local Similarity 84.7%; Pred. NO. 2e-34;
Matches 194; Conservative 0; Mismatches 33; Indels 2; Gaps 2;

QY 1 cagacctattttctgtcatttcctcaattcagaagattatattgctcacc 60
DB 3 CAGACCTTATTTTCTCTCATTTGATTCAAATTCAGAGATTATATG-GCTCAACC 61
QY 61 cacaacaagaataggcctgtcgtatgctgttaatggcaaatctgcgaaccataat 120
DB 62 CACACAAAGATAGAGCCTTCTGCTGATTTGGCTTTATGGCCAAATCTGCACATCAT 121
QY 121 tgcctgaaagggtcccaattccggttaacaacggaaccattccaaagttattggc 180
DB 122 TGC-TGAGAAAGGCTTTCCATTCTCTTTTACACCGAACCACTTCCAGGTTATGAGA 180
QY 181 cataagacgaagcaaacgaagaagaacctcaattatggggaacaa 229
DB 181 CAGTAGAAGCAGCAAAACAGAGAAATCTCCAGTTTATGCTACCA 229

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RESULT 2
BE022117      561 bp      mRNA      linear      EST 03-DEC-2001
LOCUS      sm67f12.y1 Gm-cl028 glycine max cDNA clone GENOME SYSTEMS CLONE ID:
DEFINITION      Gm-cl028-9000 5' similar to TR:022111 O22111 6-PHOSPHOGLUCONATE
ACCESSION      BE022117
VERSION      BE022117.1 GI:8284549
KEYWORDS      EST.
SOURCE      soybean.
ORGANISM      Glycine max

```

```

REFERENCE
AUTHORS      Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Corryell, V., Khanna
              A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
              Wylie, T., Underwood, R., Steptoe, M., Theising, B., Allen, M., Bowers,
              Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk
              R., Riter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
              R., Waterston, R. and Wilson, R.

```

```

TITLE      Public Soybean EST Project
JOURNAL      Unpublished (1999)
COMMENT      Contact: Shoemaker R/Public Soybean EST Project
              Public Soybean EST Project
              Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
              Tel: 314 286 1800

```

```

FEATURES
Source
    Fax: 314 286 1810
    Email: est@watson.wustl.edu
    This clone is available through: Reagen, Invitrogen Corp. 2130
    South Memorial Parkway Huntsville, AL 35801 For further information
    call: (800)-533-4363 or contact via email: cu@reagen.com
    Insert Length: 1893      Std Error: 0.00
    High quality sequence stop: 398.
    Location/Qualifiers
        1..561
            /organism="Glycine max"
            /db_xref="taxon:3847"
            /clone="GENOME SYSTEMS CLONE ID: Gm-cl028-9000"
            /clone_1lb="Gm-cl028"
            /tissue_type="roots of 'Superpod' plants"
            /lab_host="DH10B"
            /note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
            XhoI. The mRNA was isolated from roots of Glycine max
            'Superpod' plants generously donated by Dr. Gary Stacey.
            The seedlings were inoculated with Bradyrhizobium
            japonicus, strain USDA110 prior to harvest. StrataGene's
            cDNA synthesis kit (catalog number 200401) was used to
            synthesize the cDNA. First-strand synthesis was performed
            with 5-methyl dCTP, hence the ligated cDNA was
            hemimethylated. A modification of StrataGene's
            first-strand synthesis primer was used. An 'anchor'
            nucleotide (V-A-C, or G) was added to the 3' end of the
            primer (GAGAGAGAGAGAGAGAGAGACATGCTCAG(1)18V) to anchor
            the primer at the 5' end of the poly(A) tract. After
            second-strand synthesis, the cDNA ends were filled in with
            cloned Pfu DNA polymerase, ligated to EcoRI adapters and
            subsequently phosphorylated. The XhoI site within the
            first-strand synthesis primer was then restricted by
            digestion with XhoI; all XhoI sites in the cDNA would be
            protected by their hemimethylated status. The cDNA
            constructs were size-fractionated with a 500bp cutoff,
            using GIBCOBRL Life Technologies' cDNA size fractionation
            column. The column eluent was then ligated into
            StrataGene's pBluescript II SK(+) that has been digested with EcoRI
            (pBluescript II SK(+)) that has been digested with EcoRI
            and XhoI, and phosphorylated by StrataGene). Both the
            white and blue colonies appear to contain recombinant
            plasmids with cDNA inserts, based on size (n=25). This
            library was constructed by Dr. Paul Keim and Dr. Virginia
            Corryell."

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BASE COUNT      158 a      115 c      130 g      158 t
ORIGIN

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```

Query Match      60.9%; Score 139.4; DB 9; Length 561;
Best Local Similarity 81.2%; Pred. NO. 1.2e-30;
Matches 186; Conservative 0; Mismatches 41; Indels 2; Gaps 2;

```

```

QY 1 cagacctattttctgtcatttcctcaattcagaagattatattgctcacc 60
DB 7 CAGACCTTATTTTCTCTCATTTGCTTCAATTCAGGAATCAATTATG-GCTCAACC 65
QY 61 cacaacaagaataggcctgtcgtatgctgttaatggcaaatctgcgaaccataat 120
DB 66 CTCACAAAGATAGAGCCTTCTGCTGATTTGGCTTTATGGCCAAATCTAGCAGCATAT 125
QY 121 tgcctgaaagggtcccaattccggttaacaacggaaccattccaaagttattggc 180
DB 126 TGC-TGAGAAAGGCTTTCCATTCTCTTTTACACCGAACCACTTCCAAAGTTGATGAGA 184
QY 181 cataagacgaagcaaacgaagaagaacctcaattatggggaacaa 229
DB 185 CTGTGAGAACGACCAAAACAGAGAAATCTTCCAGTTTATGCTACCA 233

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```

RESULT 3
AW719787      532 bp      mRNA      linear      EST 19-APR-2000
LOCUS      AW719787
DEFINITION      LJN571104r Lotus japonicus nodule library 5 and 7 week-old Lotus

```

japonicus cDNA 5', mRNA sequence.
 AM719787
 VERSION AM719787.1 GI:7614307
 KEYWORDS EST.
 SOURCE Lotus japonicus.
 ORGANISM Lotus japonicus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae;
 Lotus.
 REFERENCE 1 (bases 1 to 532)
 AUTHORS Colebatch,G., Freund,S., Trevisakis,B and Urdavari,M.
 TITLE Lotus japonicus root nodule ESTs: tools for functional genomics
 JOURNAL Unpublished (2000)
 COMMENT Contact: Urdavari M
 Molecular Plant Nutrition
 Max Planck Institute of Molecular Plant Physiology
 Am Muehlenberg 1, 14476 Golm, Germany
 Fax: 49 331 567 8250
 Email: urdavarid@mpimp-golm.mpg.de
 Seq primer: T7
 High quality sequence stop: 532.
 Location/Qualifiers
 1..532
 /organism="Lotus japonicus"
 /cultivar="Gifu (B-129)"
 /db_xref="taxon:34305"
 /clone_idb="Lotus japonicus nodule library 5 and 7
 week-old"
 /dev_stage="5 and 7 week-old plants"
 /note="Organ: Nodule; Vector: pSPORT1; Site_1: Salt;
 Site_2: NaCl; The library was prepared using mRNA
 extracted from nodules of 5 and 7 week-old Lotus plants.
 Nodules were induced by, and contained Mesorhizobium
 strain R7A."

BASE COUNT 151 a 102 c 137 g 140 t 2 others
 ORIGIN

Query Match 49.5%; Score 113.4; DB 9; Length 532;
 Best Local Similarity 74.2%; Pred. No. 5.4e-23;
 Matches 170; Conservative 0; Mismatches 56; Indels 3; Gaps 2;

Oy 3 gacattattttctgtcattgtctcaatttcagagaaattatgctgcaccacca 62
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2 GACCTCATTTTGGTGTTCGATTCATTTTCAGCAATAATTAATGCGCTCAACCCAA 61
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Oy 63 c--aacaagataagccttgctgattgctgctgtaattgagcaaatctgcgaccataat 120
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 62 TCTTACGAGATAGGCTGCTGCTGAGCTGCTGTTATGGGCCAAATCTTGCATCAATAT 121
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Oy 121 tgcctgaaaagggcttcctccattccggttaacaacgagaaacattccaaggttatggc 180
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 122 TGC-TGAGAAGGCTTCCCATTTCTGTTTACAAACGACACATCCAAAGTTGATGAGA 180
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Oy 181 cataagacgaagcaaacacgaagaacactcaattatgagggaacaa 229
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 181 CAGTTGAACGGCGCAAAACAGAGAAACCTTCCAGTGTATGCTACCA 229
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 4
 AV406682 430 bp mRNA linear EST 23-MAY-2000
 LOCUS AV406682 Lotus japonicus young plants (two-week old) Lotus
 DEFINITION japonicus cDNA clone MML008a02_r 5', mRNA sequence.
 ACCESSION AV406682
 VERSION AV406682.1 GI:7719536
 KEYWORDS EST.
 SOURCE Lotus japonicus.
 ORGANISM Lotus japonicus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae;

Lotus.
 REFERENCE 1 (bases 1 to 430)
 AUTHORS Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
 TITLE Generation of 7137 non-redundant expressed sequence tags from a
 JOURNAL Legume, Lotus japonicus
 MEDLINE DNA Res. 7 (2), 127-130 (2000)
 COMMENT Contact: Yasukazu Nakamura
 The First Laboratory for Plant Gene Research
 Kazusa DNA Research Institute
 Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
 Email: ynakamu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
 Location/Qualifiers
 1..430
 /organism="Lotus japonicus"
 /db_xref="taxon:34305"
 /clone="MML008a02_r"
 /clone_idb="Lotus japonicus young plants (two-week old)"
 /dev_stage="young plants (two-week old)"
 /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
 XhoI; Isolate=Miyakojima MG-20"

BASE COUNT 127 a 87 c 102 g 114 t
 ORIGIN

Query Match 48.2%; Score 110.4; DB 9; Length 430;
 Best Local Similarity 73.9%; Pred. No. 4.1e-22;
 Matches 167; Conservative 0; Mismatches 56; Indels 3; Gaps 2;

Oy 6 ctattttttctgtcattgtctcaatttcagagaaattatgctgcaccacca--c 63
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1 CTCATTTTGGTGTTCGATTCATTTTCAGCAATAATTAATGCGCTCAACCAATCT 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Oy 64 aacaagataagccttgctgattgctgctgtaattgagcaaatctgcgaccataatgctc 123
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 61 TACGAGATAGGCTTGGCTGAGCTGCTGTTATGGGCCAAATCTTGCATCAATATTC 120
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Oy 124 ttgaaaagggcttcctccattccggttaacaacgagaaacattccaaggttatggccat 183
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 121 -TGAGAAGGCTTCCCATTTCTGTTTACAAACGACACATCCAAAGTTGATGAGAAG 179
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Oy 184 aagacgaagcaaacacgaagaagaacactcaattatgagggaacaa 229
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 180 TTGAACGGCGCAAAACAGAGAAACCTTCCAGTGTATGCTACCA 225
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 5
 AM695821 630 bp mRNA linear EST 20-DEC-2000
 LOCUS AM695821
 DEFINITION NF099E09ST1F1070 Developing stem Medicago truncatula cDNA clone
 NF099E09ST 5', mRNA sequence.
 ACCESSION AM695821
 VERSION AM695821.2 GI:11932865
 KEYWORDS EST.
 SOURCE barrel medic.
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliales;

Medicago.
 REFERENCE 1 (bases 1 to 630)
 AUTHORS He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
 C.J., Flores,H.R., Imman,J.T., Weller,J.W., May,G.D. and Dixon
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 JOURNAL Medicago truncatula stem library
 COMMENT Unpublished (2000)
 On Apr 14, 2000 this sequence version replaced gi:7570583.
 Contact: Dixon RA
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7302

source

1. 499
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl028-6560"
/clone_1lb="Gm-cl028"
/tissue_type="roots of 'Superpod' plants"
/lab_host="DH10B"
/note="Vector: pBluescript II Xr; Site-1: EcoRI; Site-2: XhoI; The mRNA was isolated from roots of Glycine max 'Superpod' plants generously donated by Dr. Gary Stacey. The seedlings were inoculated with Bradyrhizobium japonicus, strain USDA110 prior to harvest. Stragene's cDNA synthesis kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stragene's first-strand synthesis primer was used. An 'anchor' nucleotide (V-A-C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAGAGACTGCTCCGAG(T)18V] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA polymerase, ligated to EcoRI adapters and subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GibcoBRL Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into Stragene's pBluescript II Xr Predigested vector (pBluescript II SK(+)) that has been digested with EcoRI and XhoI, and phosphorylated by Stragene). Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=25). This library was constructed by Dr. Paul Keim and Dr. Virginia Coryell."

BASE COUNT 147 a 98 c 120 g 134 t
ORIGIN

Query Match 44.1%; Score 101; DB 9; Length 499;
Best Local Similarity 76.8%; Pred. No. 2.4e-19;
Matches 136; Conservative 0; Mismatches 40; Indels 1; Gaps 1;

QY 53 gctcaaccacaagaagaagctgtgagctgtgtaattgaaggcaaatctggca 112
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 14 GCTCAACCTTCACCAAGATATCCGCTTGCGACTGCTGTATGGGCCCAAAATCTAGCA 73

QY 113 ctcaatattgtctgaagaagctcccaattccggttaacaaggaacattccaagt 172
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 74 CTCATATTGTC-TGAGAAAGGCTTCCCATTTCTGTTTATACCGAACCCTTACCAAGGT 132

QY 173 tattggccaataagcaagcaaccgaagaagaaccttaattatgggaacaa 229
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 133 TGATGAGACTGTGGAACGACGACAAACATGAGGAATCTTCCAGTTATGCTACCA 189

RESULT 8
BF640081 435 bp mRNA linear EST 19-DEC-2000
LOCUS
DEFINITION NF027D02IN.F1025 Insect herbivory Medicago truncatula cDNA clone
ACCESSION BF640081
VERSION NF027D02IN 5', mRNA sequence.
KEYWORDS
EST. BF640081.1 GI:11904239
SOURCE
ORGANISM Medicago truncatula
barrel medic.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.
REFERENCE 1 (bases 1 to 435)
AUTHORS Korth,R., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores

TITLE
JOURNAL
COMMENT
H.R., Inman,J.T., Weller,J.W. and May,G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula insect herbivory library
Unpublished (2000)
Contact: Korth K
Dept. of Plant Pathology
University of Arkansas
217 Plant Science Building, Fayetteville, AR 72701, USA
Tel: 501 575 5191
Fax: 501 575 7601
Email: Kkorth@comp.uark.edu
Insert length: 435 Std Error: 0.00
Plate: 027 row: D column: 02
Seq primer: TCACACGAGAAACGCTAGAC.
Location/Qualifiers
1. 435
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF027D02IN"
/clone_1lb="Insect herbivory"
/tissue_type="local and systemic leaves"
/dev_stage="mature"
/note="Vector: Lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."

BASE COUNT 132 a 99 c 73 g 131 t
ORIGIN

Query Match 43.7%; Score 100; DB 10; Length 435;
Best Local Similarity 73.1%; Pred. No. 4.8e-19;
Matches 155; Conservative 0; Mismatches 55; Indels 2; Gaps 2;

QY 6 ctatttttcgtctatctgtctcaattcaggagataatgatcgctcaaccacaa 65
||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 69 CCTCATTTTTCACCTTAATCTCTTCATTTTCAGGAATATCATTTATG-GCTCAACCACTTA 127

QY 66 caagaatagccttctgtgagctgtgtaattgaaggcaaaatctgcaatcatatgtct 125
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 128 CAGGAATAGCGCTTCGGGACGCTGTATGGGCCAAATCTCGCAGCTCATATTGCG-C 186

QY 126 gaagaagcttcccaattccggttaacaaggaacattccaagttatggcataa 185
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 187 GACAAAGGATTTCCCAATTTCTGTTTATACGAAACAACATCAAGGTGACGAACCTGTG 246

QY 186 gacgaagcaacgaagaagaacctcaatt 217
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 247 GAACGAGCAAAACGAGGAGGAATCTTCCACT 278

RESULT 9
AM586409 573 bp mRNA linear EST 07-SEP-2000
LOCUS
DEFINITION ESTJ18032 MHAM Medicago truncatula/Glomus versiforme mixed EST
library cDNA clone PMHAM-5403, mRNA sequence.
ACCESSION AM586409
VERSION AM586409.1 GI:7265923
KEYWORDS
EST.
SOURCE Medicago truncatula/Glomus versiforme mixed EST library.
ORGANISM Medicago truncatula/Glomus versiforme mixed EST library
Eukaryota; mixed EST libraries.
REFERENCE 1 (bases 1 to 573)
AUTHORS Harrison,M.J., Liu,J., Peng,H., Gonzales,M., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M.
ESTs from roots of Medicago truncatula after colonization with Glomus versiforme
Unpublished (2000)
JOURNAL Contact: Maria J. Harrison
COMMENT Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401, USA

Tel: 580-223-5810
 Fax: 580-221-7380
 Email: mjharrison@noble.org
 Noble EST name: N253596
 TIGR sequence name: MDA086TK
 More information is available at:
 'http://chryslr.lamu.edu/medicago/'
 Seq primer: Skmod (CTA GAA CTA gta gat CC).
 Location/Qualifiers

FEATURES

source

1..573

/organism="Medicago truncatula/Glomus versiforme mixed EST library"

/cultivar="Medicago truncatula genotype A17"

/db_xref="taxon:119092"

/clone="PMHAM-5403"

/clone.lib="MHAM"

/tissue_type="roots colonized with Glomus versiforme"
 /dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The library was made from a mixture of RNA from each of these stages."
 /lab_host="E. coli strain XLOLR"

/note="Vector: pBluescript SK-; Site.1: EcoRI; Site.2: XhoI; cDNA was prepared from polyA+ enriched RNA from roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The cDNA was directionally ligated into the Unizap XR vector from Stralagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."

BASE COUNT

164 a 115 c 139 g 154 t
 1 others

ORIGIN

Query Match 42.0%; Score 96.2; DB 9; Length 573;
 Best Local Similarity 74.6%; Pred. No. 6.4e-18;
 Matches 147; Conservative 0; Mismatches 48; Indels 2; Gaps 2;

QY 21 attgcttcaattcaggagatattatgctgctcaaccacaagaatagccttg 80
 Db 7 AATCTCTTCAATTTTCAGGAATATCATTTATG-GCTCAACCACTTACAGATAGCGCTTG 65
 QY 81 ctgattgctgttaattggcaaaatctgacccaatatgtctgaagaagccttcca 140
 Db 66 CCGGACTGGCTGTATGCGCCAAATCTCGACATCATATTTC-CGACAAAGAGTTTCCCA 124
 QY 141 attcggtttaacacaggaacattccaaggtatgtggccataagaagcaaacacag 200
 Db 125 ATTCTGTATTATACAGAACATCAAGGTGACGAACCTGTGAAACGACGAACACAG 184
 QY 201 gaaggaaccttcaatt 217
 Db 185 GAGGGAATCTTCCACT 201

RESULT 10

BF632565

LOCUS

BF632565

367 bp mRNA linear EST 19-DEC-2000

DEFINITION

NF032C07D7JF1051 Drought Medicago truncatula cDNA clone NF032C07DT

ACCESSION

BF632565

5', mRNA sequence.

VERSION

BF632565.1 GI:11896723

KEYWORDS

EST.

SOURCE

barrel medic.

ORGANISM

Medicago truncatula

REFERENCE

Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

AUTHORS

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

TITLE

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;

COMMENT

Medicago. 1 (bases 1 to 367)

REFERENCE

1 (bases 1 to 367)

AUTHORS

Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,

TITLE

Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.

COMMENT

Expressed Sequence Tags from the Samuel Roberts Noble Foundation

JOURNAL

Medicago truncatula drought library

COMMENT

Unpublished (2000)

CONTACT

Contact: May GD

ADDRESS

Plant Biology Division

INSTITUTION

The Samuel Roberts Noble Foundation

ADDRESS

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

TELEPHONE

Tel: 580 221 7391

FAX

Fax: 580 221 7380

EMAIL

Email: gdmay@noble.org

INSERT LENGTH

Insert Length: 367 Std Error: 0.00

PLATE

Plate: 032 row: C column: 07

SEQ PRIMER

Seq primer: TCACACAGCAACACCTATGAC.

FEATURES

source

1..367

/organism="Medicago truncatula"

/db_xref="taxon:3880"

/clone="NF032C07DT"

/clone.lib="Drought"

/tissue_type="Plantlets"

/dev_stage="Pooled timepoints"

/note="Vector: Lambda Zap; Contains a mixture of entire plantlets harvested in a series of days-post-watering timepoints."

BASE COUNT

117 a 75 c 80 g 95 t

ORIGIN

Query Match 41.9%; Score 96; DB 10; Length 367;
 Best Local Similarity 75.5%; Pred. No. 7.1e-18;
 Matches 145; Conservative 0; Mismatches 45; Indels 2; Gaps 2;

QY 26 ctccaattcaggagatattatgctgctcaaccacaagaatagccttctgga 85
 Db 1 CTTCATTTTCAGGAATATCATTTATG-GCTCAACCACTTACAGATAGCGCTTCCCGCA 59
 QY 86 ttggtctgtaattggcaaaatctgacccaatatgtctgaagaagccttccaattcc 145
 Db 60 CTGGCTGTATGGGCCAAATCTCGACATCAATATTGC-CGACAAAGAGTTTCCCAATTTC 118
 QY 146 ggttaacacggaacattccaaggttattgtggccataagaagcaaacaggaaagg 205
 Db 119 TGTATTATACAGAACATCAAGGTGACGAACCTGTGAACGACGAACAGAGAGG 178
 QY 206 aaaccttcaatt 217
 Db 179 AATCTTCCACT 190

RESULT 11

AL368071

LOCUS

AL368071

430 bp mRNA linear EST 03-AUG-2000

DEFINITION

MTBA22A07F1 MTBA Medicago truncatula cDNA clone MTBA22A07 T3, mRNA

ACCESSION

AL368071

sequence.

VERSION

AL368071.1 GI:9667824

KEYWORDS

EST.

SOURCE

barrel medic.

ORGANISM

Medicago truncatula

REFERENCE

Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

AUTHORS

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

TITLE

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;

COMMENT

Medicago. 1 (bases 1 to 430)

REFERENCE

1 (bases 1 to 430)

AUTHORS

Journet, E.P., Crespeau, H., van Tulpen, D., Gouzy, J., Jaillon, O.,

TITLE

Niebel, A., Carreau, V., Chataigner, O., Kahn, D., Gianinazzi-Pearson,

JOURNAL

V. and Gamas, P.

COMMENT

Medicago truncatula ESTs from nitrogen-starved roots

REFERENCE

Genoscope, Centre National de Sequencage

AUTHORS

BP 191 91006 Evry cedex - France

TITLE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

COMMENT

Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de

Biologie Moléculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email :
Mt-est@toulouse.inra.fr Website :
http://sequence.toulouse.inra.fr/Mtruncatula.html).

FEATURES

source

1.430

/organism="Medicago truncatula"

/cultivar="Jemalong"

/db_xref="taxon:3880"

/clone="MCBA22A07"

/clone_lib="MTBA"

/tissue_type="root tips"

/dev_stage="harvested after 3 days of N-starvation"

/note="Vector: pBluescript psk; Site_1: EcoRI; Site_2:

XhoI; Plants were grown in an aeroponic chamber for 14

days on nitrogen-rich medium followed by 3 days on N-free

medium. RNA was extracted from root tips (1-3 cm). cDNA

was prepared from polyA+ enriched RNA. The cDNA was

directionally ligated into Uni-zapR vector from

Stratagene and packaged using Gigapack Gold packaging

extracts. Plasmids containing cDNA inserts were

mass-excised from phage stocks using ExAssit helper phage

and propagated in SOLR cells. Clone ordering and

sequencing was performed by the Centre National de

Sequencage (Genoscope, Evry, France)."

BASE COUNT

131 a 85 c 103 g 111 t

ORIGIN

Query Match

Best Local Similarity 75.5%; Pred. No. 7.2e-18; Length 430;

Matches 145; Conservative 0; Mismatches 45; Indels 2; Gaps 2;

QY 26 ctccaattcagagataatataatgctcgaaccacacagaagaatagccttgcgga 85

Db 2 CTTCATTTTCAGAGAAATACATTATG-GCTCAACCACTTCAAGAAATAGCGCTTGCGGA 60

QY 86 ttgctgttaatgggcaaatctgcacataatctgctgaagaaggctcccaattcc 145

Db 61 CTGGCTGTTATGGGCAAAATCTGCACCTCAATATTGC-CGACAAAGATTTCCCAATTTTC 119

QY 146 ggttaacacgaagacattcccaagtattatggccataagaagacgaagaagg 205

Db 120 TGTATTAAACAGAACACATCAAGTTGACGAACCTGTGGAACGACGAACAAAGAGG 179

QY 206 aaactcatt 217

Db 180 AAATCTTCCACT 191

RESULT 12

LOCUS BI262817 492 bp mRNA linear EST 18-JUL-2001

DEFINITION NF091D06EC1F1058 Elicited cell culture Medicago truncatula cDNA

Accession BI262817

Version BI262817.1 GI:14863469

Keywords EST.

Source barrel medic.

Organism Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;

Medicago.

1 (bases 1 to 492)

He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell

,C.U., Imman,U.T., May,G.D. and Dixon,R.A.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation

Medicago truncatula elicited cell culture library

Unpublished (2001)

Contact: Dixon RA

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Insert Length: 492 Std Error: 0.00
Plate: 091 row: D column: 06
Seq primer: TCACACAGGAACAGCTATGAC.

FEATURES

source

1.492

/organism="Medicago truncatula"

/db_xref="taxon:3880"

/clone="NF091D06EC"

/clone_lib="Elicited cell culture"

/tissue_type="Cell cultures derived from root tissues"

/dev_stage="Cell suspensions were subcultured every 14

days. Cells were induced six days after subculture"

/note="Vector: Lambda Zap; Cells were induced with yeast

cell wall extracts equivalent to 50ug/ml glucose in the

final concentration. Samples were taken at 0.5, 1, 12 and

24 hours after induction. Equal amounts of RNA from each

time point were pooled and used for mRNA isolation."

BASE COUNT

143 a 98 c 119 g 128 t

ORIGIN

Query Match 41.0%; Score 94; DB 10; Length 492;

Best Local Similarity 74.5%; Pred. No. 2.8e-17;

Matches 143; Conservative 0; Mismatches 47; Indels 2; Gaps 2;

QY 26 ctccaattcagagataatataatgctcgaaccacacagaagaatagccttgcgga 85

Db 5 CTTCATTTTCAGAGAAATACATTATG-GCTCAACCACTTCAAGAAATAGCGCTTGCGGA 63

QY 86 ttgctgttaatgggcaaatctgcacataatctgctgaagaaggctcccaattcc 145

Db 64 CTGGCTGTTATGGGCAAAATCTGCACCTCAATATTGC-CGACAAAGATTTCCCAATTTTC 122

QY 146 ggttaacacgaagacattcccaagtattatggccataagaagacgaagaagg 205

Db 123 TGTATTAAACAGAACACATCAAGTTGACGAACCTGTGGAACGACGAACAAAGAGG 182

QY 206 aaactcatt 217

Db 183 AAATCTTCCACT 194

RESULT 13

LOCUS AL382847 420 bp mRNA linear EST 03-AUG-2000

DEFINITION M8BC10C10F1 MbBC Medicago truncatula cDNA clone M8BC10C10 T3, mRNA

sequence.

Accession AL382847

Version AL382847.1 GI:9682598

Keywords EST.

Source barrel medic.

Organism Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;

Medicago.

1 (bases 1 to 420)

Journet,E.P., Crespeau,H., van-Tulnen,D., Gouzy,J., Jallion,O.,

Nielsen,A., Carreau,V., Chataigner,O., Kahn,D., Gianluigi-Pearson

,V. and Gamas,P.

Medicago truncatula ESTs from endomycorrhizal roots

Unpublished (2000)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: sequef@genoscope.cns.fr. Web : www.genoscope.cns.fr

Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de

Biologie Moléculaire des Relations Plantes-Microorganismes,

CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email :

FEATURES
source

Location/Qualifiers

Location/Qualifiers

1..420

/organism="Medicago truncatula"

/cultivar="Jemalong"

/db_xref="taxon:3880"

/clone="MTBC10C10"

/clone.lib="MTBC"

/tissue_type="arbuscular mycorrhiza"

/dev_stage="harvested 3 weeks post inoculation with Glomus intraradices"

/note="Vector: pBluescript PSK, Site 1: EcoRI; Site 2: XhoI; M. truncatula sterilised seeds were germinated for 72h at 25 C, before transplanting into a 1/3 Epiosses soil

: 2/3 calcined Terragreen mix in the presence of onion root fragments colonized by the arbuscular mycorrhizal fungus Glomus intraradices (Schenck & Smith, isolate LP8)

). The plants were watered every day and twice a week with a modified nutrient long Ashton solution without phosphate but with a high level of nitrate. After 3 weeks RNA was extracted from whole root systems. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-zap XR vector from Stratagene and packaged using GigaPack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using Exasit helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France). Note : EST may be of fungal origin."

BASE COUNT 128 a 83 c 102 g 106 t 1 others

ORIGIN

Query Match 39.1%; Score 89.6; DB 9; Length 420;

Best Local Similarity 74.6%; Pred. No. 5.6e-16;

Matches 138; Conservative 0; Mismatches 45; Indels 2; Gaps 2;

Db 1 TTTTCAGAAATACATTAAG-GCTACACCTTACAGAAATAGGCTTCGGACTGCTG 59

Qy 93 ttaatgggcaaatctggcactcaatatgttgaagaagctcccaatccggttaac 152

Db 60 TTATGGGCGCAAAATCTGCCTCAATATGTC-CGACNAAGATTTCCCAATTTCTGTTAT 118

Qy 153 aaggaaccatttccaaggttatgtggccataagaagcaagaacaggaagaacatt 212

Db 119 AACGAAACACATCAAAAGTTGACGAAACCTGTGGAACGACCAAAACAGGAGAAATCTT 178

Qy 213 caatt 217

Db 179 CCACT 183

RESULT 14

BF645919 627 bp mRNA linear EST 20-DEC-2000

LOCUS

DEFINITION

Accession

Version

Keywords

Source

Organism

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;

Medicago.

1 (bases 1 to 627)

REFERENCE

1 (bases 1 to 627)

AUTHORS

Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,

Flores, H.R., Inman, J.T., Weller, J.W., and May, G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation -

Genoscope - Centre National de Sequencage

JOURNAL
COMMENT

Center for Medicago Genomics Research

Unpublished (2000)

Contact: Dixon RA

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Tel: 580 221 7302

Fax: 580 221 7380

Email: radixon@noble.org

Insert Length: 627 Std Error: 0.00

Plate: 040 row: E column: 03

Seq primer: TCACACAGGAAACGCTATGAC.

Location/Qualifiers

1..627

/organism="Medicago truncatula"

/db_xref="taxon:3880"

/clone="NF040E03EC"

/clone.lib="Elicited cell culture"

/tissue_type="Cell cultures derived from root tissues"

/dev_stage="Cell suspensions were subcultured every 14 days. Cells were induced six days after subculture"

/note="Vector: Lambda Zap; Cells were induced with yeast cell wall extracts equivalent to 50ug/ml glucose in the final concentration. Samples were taken at 0.5, 1, 12 and 24 hours after induction. Equal amounts of RNA from each time point were pooled and used for mRNA isolation."

BASE COUNT 180 a 123 c 148 g 174 t 2 others

ORIGIN

Query Match 38.5%; Score 88.2; DB 10; Length 627;

Best Local Similarity 73.2%; Pred. No. 1.5e-15;

Matches 153; Conservative 0; Mismatches 53; Indels 3; Gaps 3;

Qy 11 tttctgtcatttgcctcaaatltaagaagattatgctcaacc-cacacaag 69

Db 3 TTTTTCACCTAATCTTCATATTTTCAGAAATACATATGCTTCACCACTTACAA 62

Qy 70 aatagccttgcgtgatttg-cgttaetggcacaatctgcaatcctaatatgttga 128

Db 63 AATAGGCTTGGCGGACTGCTGTTATGGCCAAATCTGCCTCAATATTTGC-CGAC 121

Qy 129 aaggcttcccaattcctglttaacaaggaacatttccaaggttatgggcataagac 188

Db 122 AAGGATTTCCCAATTTCTGTTATAACAGAACACATCAAGCTTGACGAATGTGAA 181

Qy 189 gaagcaaccaggaaggaacattcaat 217

Db 182 CGAGCAAAACAGAGGAATCTTCACCT 210

RESULT 15

AL367204 337 bp mRNA linear EST 03-AUG-2000

LOCUS

DEFINITION

Accession

Version

Keywords

Source

Organism

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;

Medicago.

1 (bases 1 to 337)

REFERENCE

1 (bases 1 to 337)

AUTHORS

Journet, E.P., Crespeau, H., van Tuinen, D., Gouzy, J., Jaillon, O.,

Niebel, A., Carreau, V., Chabagnier, O., Kahn, D., Gianinazzi-Pearson

, V. and Gamas, P.

Medicago truncatula ESTs from nitrogen-starved roots

Unpublished (2000)

CONTACT: Genoscope

Genoscope - Centre National de Sequencage

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2002, 15:37:00 ; Search time 5254.53 Seconds

(without alignments)
927.939 Million cell updates/sec

Title: us-09-300-482-1

Perfect score: 233
Sequence: 1 gttttgcagcttagtagaac.....ttgacaagggtattgttg 233

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :
1: GenEmbl:*
2: gb_hhg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_to:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: gb_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_ov:*
22: em_or:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_in:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
1	131.6	56.5	1904	AB029456
2	131.6	56.5	1924	AB029455
3	131.6	56.5	1956	AB029454
4	106.8	45.8	59348	H0811E11
5	106.8	45.8	121690	OSJN00125
6	106.8	45.8	151889	OSJN00053
7	106.6	45.8	1785	MSU18238
8	101.8	43.3	1689	STG6PDH
9	100.8	43.3	1957	AF012863
10	97	41.6	1821	NTTCG9
11	96	41.2	1848	AF012862
12	95.4	40.9	1810	AY065054
13	95.4	40.9	1852	NTTCG6
14	95.4	40.9	1862	ATRH010970
15	93.8	40.3	1690	ATRH010971
16	78	33.5	63604	AP000381
17	77.8	33.4	1777	AF097663
18	74.6	32.0	14323	AB015470
19	39	16.7	37184	HS09PD4
20	39	16.7	180008	AC022962
21	38.4	16.5	168106	AC099540
22	36.8	15.8	110000	LMFCHR34_11
23	36.8	15.8	110000	LMFCHR34_12
24	35.8	15.4	117840	AL162400
25	35.8	15.4	147990	AC026144
26	35.4	15.2	63441	AL356502
27	35	15.0	166239	AC078965
28	35	15.0	168822	AC007511
29	34.8	14.9	164012	AC009386
30	34.8	14.9	187258	AC018976
31	34.6	14.8	597	AX141463
32	34.6	14.8	2945	AF269329
33	34.6	14.8	2945	AX144649
34	34.6	14.8	3825	AF269754
35	34.6	14.8	3825	AX145072
36	34.6	14.8	182727	AC068066
37	34.4	14.8	10286	AX277850
38	34.4	14.8	10286	AX323533
39	34.4	14.8	174132	AC095090
40	34.4	14.8	174344	AC094634
41	34.2	14.7	150876	AC108761
42	34.2	14.7	163166	AL356632
43	34	14.6	137480	OSJN00219
44	34	14.6	180844	AL606536
45	33.8	14.5	93830	AC097789

ALIGNMENTS

RESULT	1	1904 bp	mrna	linear	PLN 06-OCT-2000
AB029456	LOCUS	AB029456	1904 bp	mrna	linear
DEFINITION	Triticum aestivum g6pdh mRNA for glucose-6-phosphate dehydrogenase, complete cds, clone:Ta9pd3.				
ACCESSION	AB029456				
VERSION	AB029456.1	GI:8918505			
KEYWORDS	glucose-6-phosphate dehydrogenase.				
SOURCE	Triticum aestivum (cultivar:Chinese spring, isolate:root) seedling CDNA to mRNA, clone:Ta9pd3.				
ORGANISM	Triticum aestivum				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticaceae; Triticum.				
AUTHORS	Nemoto, Y., Kawakami, N. and Sasakuma, T.				
TITLE	Isolation of novel early salt-respondering genes from wheat (Triticum aestivum L.) by differential display				
JOURNAL	Theor. Appl. Genet. 98, 673-678 (1999)				
REFERENCE	2 (sites)				
AUTHORS	Nemoto, Y. and Sasakuma, T.				
TITLE	Specific expression of glucose-6-phosphate dehydrogenase (G6PDH) gene by salt stress in wheat (Triticum aestivum L.)				

JOURNAL Plant science (Shannon, Ireland) 158 (1-2), 53-60 (2000)
PUBMED 10996244
REFERENCE 3 (bases 1 to 1904)
AUTHORS Nemoto, Y.
TITLE Direct Submission
JOURNAL Submitted (01-JUL-1999) Yasue Nemoto, Yokohama City University,
Kihara Institute for Biological Research, Maiooka, Totsuka, Yokohama
244-0813, Japan (E-mail:nemoto@yokohama-cu.ac.jp,
Tel:81-45-820-1902, Fax:81-45-820-1901)
FEATURES
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RFANRLFLPLNRNDVNIQIVFREDFGDRGDFYQYGIIRIDYIIONHLQVFCIVA
MEKPVSLKPEHIDREKVKVLOSVPNIDEEVYLGQIOGFKEDPTPDDSTPTFASIV
LRVHNERGVPFLIKAGKALNSKAEIRVQFDKPDIFCKKQGNENRVILOPSE
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Best Local Similarity 76.3%; Pred. No. 3.1e-29;
Matches 177; Conservative 0; Mismatches 49; Indels 6; Gaps 1;
QY 2 ttcttgcaatgtagaataatgtagtgcctccatagataggttggaagattgagta 61
DB 447 TTCTTGCAATGATAAATAATGTCAGTGTCTCATATACAGTGAGAGAGGTTTGA AAAA 506
QY 62 ttgaatgaggaatctctgtagttagaagctcagaacaaatgactcggaagctacccg 121
DB 507 CTGAACAAGGAATAATCATGATATAGATGTCA-----AACAACTCAGGAAGCTCCCGT 560
QY 122 agatatattatcttgtagctcctcatgtagtccatcgaatagcgaatagatagata 181
DB 561 AGGCTCTTTATTTTGGCATTTGCTCCTCATCTGCTACCTTCAGTGAGCAAAATGATCCGA 620
QY 182 tcatatgcatgagtcacatcttcacacacgggttgacaaaggtttatgttg 233
DB 621 ACATATTGATGATGCCAACTCTCGCGCTGATGAGCTAAGATATTGTGG 672
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LOCUS Triticum aestivum g6pdh mRNA for glucose-6-phosphate dehydrogenase,
DEFINITION complete cds, clone:Tagpd2.
ACCESSION AB029455
VERSION AB029455.1 GI:8918503
KEYWORDS glucose-6-phosphate dehydrogenase.
SOURCE Triticum aestivum (cultivar:Chinese spring, isolate:root) seedling
CDNA to mRNA, clone:Tagpd2.
Triticum aestivum
* ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE 1 (sites)
AUTHORS Nemoto, Y., Kawakami, N. and Sasakuma, T.
TITLE Isolation of novel early salt-respondering genes from wheat (Triticum
aestivum L.) by differential display
JOURNAL Theor. Appl. Genet. 98, 673-678 (1999)
REFERENCE 2 (sites)
AUTHORS Nemoto, Y. and Sasakuma, T.
TITLE Specific expression of glucose-6-phosphate dehydrogenase (G6PDH)
gene by salt stress in wheat (Triticum aestivum L.)
JOURNAL Plant science (Shannon, Ireland) 158 (1-2), 53-60 (2000)
PUBMED 10996244
REFERENCE 3 (bases 1 to 1924)
AUTHORS Nemoto, Y.
TITLE Direct Submission
JOURNAL Submitted (01-JUL-1999) Yasue Nemoto, Yokohama City University,
Kihara Institute for Biological Research, Maiooka, Totsuka, Yokohama
244-0813, Japan (E-mail:nemoto@yokohama-cu.ac.jp,
Tel:81-45-820-1902, Fax:81-45-820-1901)
FEATURES
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A"
BASE COUNT 545 a 417 c 475 g 487 t
ORIGIN
Query Match 56.5%; Score 131.6; DB 8; Length 1924;
Best Local Similarity 76.3%; Pred. No. 3.1e-29;
Matches 177; Conservative 0; Mismatches 49; Indels 6; Gaps 1;
QY 2 ttcttgcaatgtagaataatgtagtgcctccatagataggttggaagattgagta 61
DB 445 TTCTTGCAATGATAAATAATGTCAGTGTCTCATATACAGTGAGAGAGGTTTGA AAAA 514
QY 62 ttgaatgaggaatctctgtagttagaagctcagaacaaatgactcggaagctacccg 121
DB 515 CTGAACAAGGAATAATCATGATATAGATGTCA-----AACAACTCAGGAAGCTCCCGT 568
QY 122 agatatattatcttgtagctcctcatgtagtccatcgaatagcgaatagatagata 181
DB 569 AGGCTCTTTATTTTGGCATTTGCTCCTCATCTGCTACCTTCAGTGAGCAAAATGATCCGA 628
QY 182 tcatatgcatgagtcacatcttcacacacgggttgacaaaggtttatgttg 233
DB 629 ACATATTGATGATGCCAACTCTCGCGCTGATGAGCTAAGATATTGTGG 680
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LOCUS	AB029454	1956 bp	mRNA	linear	PLN 06-OCT-2000
DEFINITION	Triticum aestivum 6pDh mRNA for glucose-6-phosphate dehydrogenase, complete cds, clone:Tagpdl.				
ACCESSION	AB029454				
VERSION	AB029454.1 GI:8918501				
KEYWORDS	glucose-6-phosphate dehydrogenase.				
SOURCE	Triticum aestivum (cultivar:Chinese Spring, isolate:root) seedling cDNA to mRNA, clone:Tagpdl.				
ORGANISM	Triticum aestivum				
REFERENCE	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Triticum.				
AUTHORS	1 (sites)				
TITLE	Nemoto,Y., Kawakami,N. and Sasakuma,T.				
JOURNAL	Isolation of novel early salt-respondering genes from wheat (Triticum aestivum L.) by differential display				
REFERENCE	Theor. Appl. Genet. 98, 673-678 (1999)				
AUTHORS	2 (sites)				
TITLE	Nemoto,Y. and Sasakuma,T.				
JOURNAL	Specific expression of glucose-6-phosphate dehydrogenase (6pDh) gene by salt stress in wheat (Triticum aestivum L.)				
PUBMED	Plant science (Shannon, Ireland) 158 (1-2), 53-60 (2000)				
AUTHORS	10996244				
TITLE	3 (bases 1 to 1956)				
JOURNAL	Nemoto,Y.				
REFERENCE	Direct Submission				
AUTHORS	Submitted (01-JUL-1999) Yasue Nemoto, Yokohama City University, Kihara Institute for Biological Research, Maoka, Totsuka, Yokohama				
TITLE	244-0813, Japan (E-mail:nemoto@yokohama-cu.ac.jp, Tel.:81-45-820-1902, Fax:81-45-820-1901)				
JOURNAL	Location/Qualifiers				
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	SPTRSLGWTIRVYERKPGRIIDSEELSOLGELFEEDOLYRIDHYLKLNOVLIVL				
	RPNRLALPLMNRNVNINIGIVREDGCTGGRGCEPDYGTIRIIONHLLQVFCVLA				
	MEKVSLSKPEHIREKVKLVQSVNPIDEEVYLAQYTGKIDDPVPDSSNTPFASIV				
	LRVHNERWEGVPTLKAGKALNSRKARIVQFKVNPDEDFCKRKGNEVIRLRDSE				
	AMWKLKVPKPGLEMTAGESELDLSYMRVQDVKIPAYRELIDITIGGQDQHFVRD				
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Best Local Similarity	76.3%; Pred. No. 3,1e-29;				
Matches 177;	Conservative	0;	Mismatches	49;	Indels
					Gaps 1;
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OY	62	ttgaatggcgcaatctctcgagtagtagagaactcagaanaacaatgactcgggaagctaccgc	121		
DB	516	CTGAACAAGGAATATCGATTATGAGTATGCA-----AACCAACTCGGAAGCTCCGCT	569		

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Db	570	AGGCGCTTTTATTTTGGCATTGGCTCCATCTGTCTACCTTAGTCGTCAAAATATATCCGA	629
QY	182	tcaatttcattgaatgcattcttcacacacccggttgacaaaggtattatgty	233
Db	630	ACATATTGCAATGACATCCAACTTCTGCGCTGGATGAGCACTAAGTATTATTGTTG	681
RESULT	4		
LOCUS	H0811E11	59348 bp	DNA linear
DEFINITION	Oryza sativa genomic DNA, chromosome 4, BAC clone: H0811E11,		PLN 20-SEP-2000
ACCESSION	AL442114		
VERSION	AL442114.1		
KEYWORDS	complete sequence.		
SOURCE			
ORGANISM	Oryza sativa.		
REFERENCE	Oryza sativa.		
AUTHORS	Euharvota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.		
REFERENCE	1 (bases 1 to 59348)		
AUTHORS	Han,B., Feng,Q., Huang,Y.C., Zhou,B., Chen,Z.H., Li,Y., Zhu,J.J., Tang,Y.S., Zhao,Q., Liu,Y.L., Mu,J., Yu,Z., Pan,D.L., Chen,L., Wang,Q.J., Zhang,L., Lu,Y.Q., Yu,S.L., Zhu,J., Liu,X.H., Hu,X., Lei,H.Y., Zhang,Y.J., Wang,R., Li,C., Lu,Y., Chen,X.C., Zhang,Y., Hu,H., Jia,P.X., Li,T., Qian,Y.M., Ying,K. and Hong,G.F.		
TITLE	Oryza sativa indica (Guangluai4) genomic DNA, chromosome 4, BAC clone: H0811E11		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 59348)		
AUTHORS	Hong,G.F.		
JOURNAL	Direct Submission		
COMMENT	Submitted (18-SEP-2000) Hong G.F., National Center for Gene Research, Chinese Academy of Sciences, 500# Caobao Road, Shanghai 200233, CHINA		
FEATURES	Genes were predicted from the combined results of the following: GenScan1.0 and geneMark1.0. The predicted proteins were searched against NCBI NonRedundant Protein database, nr.		
SOURCE	Location/Qualifiers		
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exon	/chromosome="4"		
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Oy 75 tctctgagatagagactcagaacaacatgactcggaaagctaccgcagatattatt 134
Db 33763 TTTCAGAGTATGAGAGTCA-----AACAAATCAGAAAGCCCTCGCAGAGCTCTTATT 33816
Oy 135 tggcattgcctccatcagtcctaccatcagatgcgagatgataatcatattgcacba 194
Db 33817 TGGCATTGGCTCCATCTGCTACCTTCAGTGCAGAAATGATCAGAACATATTTGATGA 33876
Oy 195 gtccatct 202
Db 33877 ATCCATGT 33884

RESULT 5
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LOCUS OSJN00125 121690 bp DNA linear HTG 27-SEP-2001
DEFINITION Oryza sativa chromosome 4 clone OJ1672_A04, *** SEQUENCING IN
PROGRESS ***, in ordered pieces.
ACCESSION AL606998
VERSION AL606998.1 GI:15799239
KEYWORDS HTG; HTGS, PHASE2.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 121690)
Fu, G., Wang, S. Y., Ren, S. X., Lv, G., Lin, W., Gu, W. Q., Zhu, G. F.,
Tu, Y. F., Jia, J., Yin, H. F., Zhang, Y., Cai, Z., Chen, J., Kang, H.,
Chen, X. Y., Shao, C. Y., Sun, Y., Hu, Q. P., Zhang, X. L., Zhang, W.,
Wang, L. J., Ding, C. W., Sheng, H. H., Gu, J. L., Chen, S. T., Ni, L.,
Zhu, F. H., Han, B., Feng, Q., Huang, Y. C., Li, Y., Zhu, J. J., Zhao, Q.,
Hu, X., Liu, Y. L., Mu, J., Yu, Z., Chen, L., Fan, D. L., Meng, Q. J.,
Zhang, L., Lu, Y. Q., Yu, S. L., Liu, X. H., Lu, T. T., Zhang, Y. J., Lu, Y.,
Li, C., Li, T., Zhang, Y., Hu, H., Jia, P. X., Qian, Y. M., Ying, K.,
Zhou, B., Chen, Z. H., Hao, P., Zhang, L., Wu, M., Zhang, R. Q., Guan, J. P.
and Hong, G. F.
Direct Submission
Submitted (28-JUL-2000) Han Bin, National Center for Gene Research,
Chinese Academy of sciences, 500# Cao Bao Road, Shanghai 200233,
CHINA. E-mail enquiries: bhan@ncgr.ac.cn. Clone requests:
bhan@ncgr.ac.cn
Oryza sativa japonica (niponbare) genomic DNA, chromosome 4, BAC
clone: OJ1672_A04.
Web site: http://www.ncgr.ac.cn
----- Summary Statistics
Assembly program: phrap

* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

FEATURES
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Db 62621 TTTCAGAGTATGAGAGTCA-----AACAAATCAGAAAGCCCTCGCAGAGCTCTTATT 62674
Oy 135 tggcattgcctccatcagtcctaccatcagatgcgagatgataatcatattgcacba 194
Db 62675 TGGCATTGGCTCCATCTGCTACCTTCAGTGCAGAAATGATCAGAACATATTTGATGA 62734
Oy 195 gtccatct 202
Db 62735 ATCCATGT 62742

RESULT 6
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LOCUS OSJN00053/c 151889 bp DNA linear HTG 11-SEP-2001
DEFINITION Oryza sativa chromosome 4 clone OSJNba0081L15, *** SEQUENCING IN
PROGRESS ***, in ordered pieces.
ACCESSION AL606623
VERSION AL606623.1 GI:15594082
KEYWORDS HTG; HTGS, PHASE2.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 151889)
Fu, G., Wang, S. Y., Ren, S. X., Lv, G., Lin, W., Gu, W. Q., Zhu, G. F.,
Tu, Y. F., Jia, J., Yin, H. F., Zhang, Y., Cai, Z., Chen, J., Kang, H.,
Chen, X. Y., Shao, C. Y., Sun, Y., Hu, Q. P., Zhang, X. L., Zhang, W.,
Wang, L. J., Ding, C. W., Sheng, H. H., Gu, J. L., Chen, S. T., Ni, L.,
Zhu, F. H., Han, B., Feng, Q., Huang, Y. C., Li, Y., Zhu, J. J., Zhao, Q.,
Hu, X., Liu, Y. L., Mu, J., Yu, Z., Chen, L., Fan, D. L., Meng, Q. J.,
Zhang, L., Lu, Y. Q., Yu, S. L., Liu, X. H., Lu, T. T., Zhang, Y. J., Lu, Y.,
Li, C., Li, T., Zhang, Y., Hu, H., Jia, P. X., Qian, Y. M., Ying, K.,
Zhou, B., Chen, Z. H., Hao, P., Zhang, L., Wu, M., Zhang, R. Q., Guan, J. P.
and Hong, G. F.
Direct Submission
Submitted (28-JUL-2000) Han Bin, National Center for Gene Research,
Chinese Academy of sciences, 500# Cao Bao Road, Shanghai 200233,
CHINA. E-mail enquiries: bhan@ncgr.ac.cn. Clone requests:
bhan@ncgr.ac.cn
Oryza sativa japonica (niponbare) genomic DNA, chromosome 4, BAC
clone: OSJNba0081L15.
Web site: http://www.ncgr.ac.cn
----- Summary Statistics
Assembly program: phrap

* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

FEATURES
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Best Local Similarity 77.1% Pred. No. 8,1e-22;
Matches 145; Conservative 0; Mismatches 37; Indels 6; Gaps 1;

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QY 195 gtccatct 202
Db 22462 ATCCATGCT 22455

RESULT 7
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LOCUS Medicago sativa glucose-6-phosphate dehydrogenase mRNA, complete
DEFINITION cds
ACCESSION U18238
VERSION U18238.1 GI:603218
KEYWORDS alfalfa.
SOURCE Medicago sativa subsp. sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

REFERENCE 1 (bases 1 to 1785)
AUTHORS Fahrendorf, T., Ni, W., Shorrosh, B.S. and Dixon, R.A.
TITLE Stresses responses in alfalfa (Medicago sativa L.) XX.
Transcriptional activation of oxidative pentose phosphate pathway genes at the onset of the isoflavonoid phytoalexin response
JOURNAL Plant Mol. Biol. 28 (5), 885-900 (1995)
MEDLINE 95367649
AUTHORS Fahrendorf, T.
TITLE 2 (bases 1 to 1785)
REFERENCE Direct Submission
AUTHORS Submitted (06-DEC-1994) Theo Fahrendorf, Samuel Roberts Noble Foundation, Plant Biology Division, 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
JOURNAL Location/Qualifiers

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polyA_site

BASE COUNT 551 a 306 c 396 g 532 t
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Best Local Similarity 66.1%; Pred. No. 1,1e-21;

Matches 154; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
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Db 346 GTTTTACCAATTTGTTAAATATGTAAGTGCCCTTATGATTTCTGAAAGAGATTTCGCTT 405
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QY 121 cagattatttatttgcatctgctccatcagtcagtcacatgatatgcagatgataag 180
Db 466 GAGGCTTTCTATCTTGACATTCCTCCTTCAGTGTATCCATCCGTTTCAGAGATGATCA 525
QY 181 atcatattcagatgacatcttcacacacccggttggaaggttatgtgtg 233
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DEFINITION X74421
ACCESSION X74421.1 GI:471344
VERSION X74421.1 GI:471344
KEYWORDS cytosolic enzyme; g6pdh gene; glucose-6-phosphate dehydrogenase; oxidative pentose phosphate pathway.
SOURCE potato.
ORGANISM Solanum tuberosum

REFERENCE 1 (bases 1 to 1689)
AUTHORS von Schaewen, A.
TITLE Direct Submission
JOURNAL Submitted (30-JUN-1993) A. von Schaewen, Universitaet Osnabrueck Pflanzenphys., Barbarastr 11, 49069 Osnabrueck, FRG
REFERENCE 2 (bases 1 to 1689)
AUTHORS Greave, K., von Schaewen, A. and Scheible, R.
TITLE Purification, characterization, and cDNA sequence of glucose-6-phosphate dehydrogenase from potato (Solanum tuberosum L.)
JOURNAL Plant J. 5 (3), 353-361 (1994)
MEDLINE 94236152

FEATURES
source
Location/Qualifiers

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 OY 122 agattatttatttggcaatgcctccatcgaactgaaccatcagatagtggaagttgataaga 181
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DEFINITION	Nicotiana tabacum mRNA for cytosolic glucose-6-phosphate dehydrogenase TCG9.	
ACCESSION	AJ001770	
VERSION	AJ001770.1	GI:3021509
KEYWORDS	glucose-6-phosphate dehydrogenase.	
SOURCE	common tobacco.	
ORGANISM	Nicotiana tabacum	
REFERENCE	Euraryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.	
AUTHORS	1 (bases 1 to 1821) Wendt,U.K., Hauschild,R., Lange,C., Pletzema,M., Wenderoth,I. and von Schaewen,A.	
TITLE	Evidence for functional convergence of redox regulation in G6PDH isoforms of cyanobacteria and higher plants	
JOURNAL	Plant Mol. Biol. 40 (3), 487-494 (1995)	
MEDLINE	99364543	
REFERENCE	2 (bases 1 to 1821) von Schaewen,A.	
AUTHORS	Direct Submission	
TITLE	Submitted (18-sep-1997) von Schaewen A., Plant Physiology, University Osnabrueck, Barbarastr. 11, D-45069 Osnabrueck, GERMANY	
JOURNAL	Location/Qualifiers	
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Query Match	41.6%	Score 97;	DB 8;	Length 1821;
Best Local Similarity	63.5%	Pred. No. 8.8e-19;		
Matches 148; Conservative	0;	Mismatches 85;	Indels 0;	Gaps 0

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OY	61	attgaatgaagccaatcctctgagtatgagacttcgaataacaaatgctcgggaagctaccg	120
Db	444	ACTGGACAAAGGCTATAGCTGAGCACGAAATTGCCAAAAATAGCACAGAAGGTCATCCAG	503
OY	121	caaatattattatttggcatctgcctccatcagctccaccatcagatcggagaatagaag	180
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OY	181	atcatatgtcgttgagtcacatcttcaacacacgggttgacaagggattatctgtg	233
Db	564	AAATTAAGTATGAAACAATATGATCTTGGTGAGTGGAGCTGGCATATGTTGGTG	616

RESULT	11
LOCUS	AF012862
DEFINITION	AF012862 1848 bp mRNA linear PLN 03-SEP-1997
ACCESSION	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1
VERSION	(CG6PDI1) mRNA, complete cds.
	AF012862
	AF012862.1 GI:2352920

SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE
parsley.	<i>Petroselinum crispum</i>			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Petroselinum.			
	1 (bases 1 to 1848)			
	Batz,O., Logemann,E., Reinhold,S. and Mahlbrock,K.			
	Extensive reprogramming of cellular metabolism by fungal elicitor of infection in parsley suggests a new perception of 'defense-related' genes			

JOURNAL	Unpublished
REFERENCE	2 (Bases 1 to 1848)
AUTHORS	Batz,O., Logemann,E. and Hahlbrock,K.
TITLE	Direct Submission
JOURNAL	Submitted (08-JUL-1997) Biochemistry, MPI f. Zuechtungsforschung, Carl-von-Linne-Weg 10, Cologne, NRW 50829, Germany
FEATURES	Location/Qualifiers

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source	Location/Qualifiers
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Query Match	41.28	Score 96	DB 8	Length 1848
Best Local Similarity	63.48	Pred. No.	1.8e-18	
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RESULT	LOCUS	DEFINITION	VERSION	KEYWORDS	SOURCE	ORGANISM
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	AY065054	Arabidopsis thaliana AT3g7300/K17E12.12	1810 bp	mrna	linear	PLN 07-JAN-2002
	AY065054.1	Arabidopsis thaliana AT3g7300/K17E12.12	1810 bp	mrna	linear	PLN 07-JAN-2002
	FLI CDNA	Arabidopsis thaliana AT3g7300/K17E12.12	1810 bp	mrna	linear	PLN 07-JAN-2002
	thale cress	Arabidopsis thaliana AT3g7300/K17E12.12	1810 bp	mrna	linear	PLN 07-JAN-2002
	Arabidopsis thaliana	Arabidopsis thaliana AT3g7300/K17E12.12	1810 bp	mrna	linear	PLN 07-JAN-2002

REFERENCE
AUTHORS
 Eukaryote: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
 Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:
 Rosidae: eurosoids II: Brassicales; Brassicaceae; Arabidopsis.
 1 (pages 1 to 1810)
 Cheuk, R., Chen, H., Kim, C. J., Koesema, E., Meyers, M. C., Banb, J.,
 Bowser, L., Carninci, P., Chang, E., Dale, J. M., Goldsmith, A. D.,
 Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G.,
 Kawai, J., Lam, B., Lee, J. M., Lin, J., Miranda, M., Narusaka, M.,
 Nguyen, M., Onodera, C. S., Palm, C. J., Quach, H. L., Sakurai, T.,
 Satou, M., Seki, M., Southwick, A., Tang, C. C., Toitumi, M., Wu, H. C.,
 Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R. W.,
 Theologis, A. and Ecker, J. R.

TITLE	JOURNAL	REFERENCE	AUTHORS
Arabidopsis cDNA clones	Unpublished	2 (pages 1 to 1810)	Cheuk, R., Chen, H., Kim, C. J., Koeseema, E., Meyers, M. C., Banh, J., Bower, L., Carninci, P., Chang, E., Dale, J. M., Goldstein, A. D., Hayashizaki, Y., Ishida, J., Jones, T., Kamaya, A., Kellin-Neumann, G., Kawaji, T., Lam, B., Lee, J. M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Oondera, C. S., Palm, C. J., Quach, H. L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C. C., Ioriutti, M., Wu, H. C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R. W., Theologis, A. and Eckert, J. R.
Title	Journal	Submitted (30-Nov-2001)	Direct Submission
		(Signal), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA	
COMMENT			Riken Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : "RIKEN Arabidopsis Full-length cDNA") : Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamaya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGENC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Cheuk, R., Chen, H., Kim, C.J., Kosemea, E., Meyers, M.C., Shinn, P., Bant, J., Bowser, L.,

EuKaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids. 1 (bases 1 to 1862)
Wendt, U.K., Hauschild, R., Lange, C., Pietersma, M., Wenderoth, I. and von Schaeven, A.
Evidence for functional convergence of redox regulation in G6PDH isoforms of cyanobacteria and higher plants
Plant Mol. Biol. 40 (3), 487-494 (1999)
99364543
2 (bases 1 to 1862)
von Schaeven, A.
Direct Submission
Submitted (04-SEP-1998) von Schaeven A., Plant Physiology, University Osnabrueck, Barbarastrasse 11, D-49069 Osnabrueck, GERMANY

FEATURES
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Best Local Similarity 63.1%; Pred. No. 2.7e-18;
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DB 354 GTTTCCTAAAGCTGATTAGATAGTGTGAGCTTATGATTCGAGGAAGCGTTTAAAG 413
QY 61 attgaatgaagaacatctcgaatagacttgaagaacaatgactcgggaagctaacg 120
DB 414 ATTAGCAAGGCGATTTTGGAGACGAGATATTAAAGACTGCGAAGGATCTTCGAG 473
QY 121 cagattatttatttgcattgcctcatcagtcataccatcagatctgagagatgaag 180
DB 474 GAGATTGTTTATCTTGCACTTCCTCGTCTGATACCTCCCTGTAAGCAAGATGATCA 533
QY 181 atcatattgcagagatcattctcacacacccggttggaacaggttatctgtc 233
DB 534 GGCATGGTGCACATCAACAAATCTGATCTTGATGAGACTGATGTTGTGG 586

RESULT 15
ATH010971
LOCUS 1690 bp mRNA linear PLN 17-AUG-1999
DEFINITION Arabidopsis thaliana mRNA for cytosolic glucose-6-phosphate
1-dehydrogenase ACG12.
ACCESSION AJ010971
VERSION AJ010971.1 GI:5732196
KEYWORDS acg12 gene; glucose-6-phosphate 1-dehydrogenase.
SOURCE

ORGANISM Arabidopsis thaliana
EuKaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids. 1 (bases 1 to 1862)
Wendt, U.K., Hauschild, R., Lange, C., Pietersma, M., Wenderoth, I. and von Schaeven, A.
Evidence for functional convergence of redox regulation in G6PDH isoforms of cyanobacteria and higher plants
Plant Mol. Biol. 40 (3), 487-494 (1999)
99364543
2 (bases 1 to 1862)
von Schaeven, A.
Direct Submission
Submitted (04-SEP-1998) von Schaeven A., Plant Physiology, University Osnabrueck, Barbarastrasse 11, D-49069 Osnabrueck, GERMANY

FEATURES
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Search completed: July 3, 2002, 05:07:00
Job time: 48600 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 3, 2002, 01:10:45 ; Search time 796.36 Seconds

(without alignments)
502.337 Million cell updates/sec

Title: US-09-300-482-1

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Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	97	41.6	1915	21	AAC47923	Arabidopsis thaliana
2	34.6	14.8	597	22	AAH52396	S. epidermidis ope
3	34.6	14.8	2945	22	AAH54007	S. epidermidis gen
4	34.6	14.8	3825	22	AAH54430	S. epidermidis gen
5	34.4	14.8	10286	22	AAH54308	Chemically pretrea
6	31.8	13.6	621	22	AAH31486	Human olfactory re
7	31.6	13.6	621	22	AAH32502	Human olfactory re
8	31.6	13.6	278	21	AAH01024	Human colon cancer
9	31.4	13.5	13376	24	ABJ32583	Human Immune syste

10	31.2	13.4	4418	18	AAV74765	Staphylococcus aur
11	31	13.3	54863	22	AAK86025	Human Immune/Haema
12	31	13.3	54877	22	AAK86026	Human Immune/Haema
13	30.6	13.1	661	23	AAH71803	DNA encoding novel
14	30.6	13.1	925	22	AAI97683	Human neuroblastom
15	30.6	13.1	2322	24	ABF98851	Mouse ischaemic co
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17	30.6	13.1	4237	21	AAH78647	Human ORFX ORF2202
18	30.6	13.1	12468	22	AAH77300	Human Immune/Haema
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26	29.8	12.8	5280	18	AAV74855	Staphylococcus aur
27	29.8	12.8	5631	20	AAH85506	DNA encoding. Sac
28	29.8	12.8	6920	22	AAH24300	Legionella pneumop
29	29.8	12.8	7655	16	AAH86896	S. cerevisiae fks1
30	29.8	12.8	26997	22	AAH46747	Tumour suppressor
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32	29.6	12.7	13788	22	ABA19999	Human nervous syst
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35	29.4	12.6	3271	23	ABL03784	Drosophila melanog
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38	29.4	12.6	14335	22	AAH28524	Genomic fragment #
39	29.4	12.6	44014	23	ABL02654	Drosophila melanog
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41	29.2	12.5	687	22	AAH32558	Human genomic DNA
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ALIGNMENTS

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AC 18-OCT-2000 (first entry)

DT XX

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 55610.

XX XX

XX Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

XX XX

OS Arabidopsis thaliana.

XX XX

PN EP1033405-A2.

XX XX

PD 06-SEP-2000.

XX XX

PF 25-FEB-2000; 2000EP-0301439.

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25-FEB-1999; 99US-0121825.

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PR 09-MAR-1999; 99US-0123548.

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```
XX Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
PT useful for vaccinating against infections, e.g. endocarditis -
PS Claim 8; Page 921-922; 2188pp; English.
XX
XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
CC (I) and (II) can have antibacterial activity and therefore can be used
CC in vaccination. The nucleic acids (I) may be used to produce the
CC S. epidermidis polypeptides (II) via the production of vectors
CC containing them which are used to produce hosts cells which express the
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC used to vaccinate subjects and to raise antibodies against the bacteria.
CC The polypeptides may also be used to assay for other inhibitors of their
CC activity and therefore identify compounds that may be used for the
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
CC AAH55090 represent specifically claimed S. epidermidis genomic DNA
CC polynucleotide sequences from the present invention. AAH55091 to
CC AAH55098 represent oligonucleotide sequences and primers which are used
CC in the exemplification of the present invention.
CC N.B. The present invention specifically claims all the polynucleotide
CC sequences given in the sequence listing of the present specification,
CC however the sequence listing only goes up to SEQ ID NO:4454 so even
CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
CC no sequences are present for SEQ ID NO:4455 to 4464.
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Query Match      14.8%; Score 34.6; DB 22; Length 2945;
Best Local Similarity 61.8%; Pred. No. 0.25;
Matches 55; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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RESULT 4
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DT 03-SEP-2001 (first entry)
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KW Staphylococcus epidermidis SRI strain; infection; diagnosis;
KM vaccination; endocarditis; ds.
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OS Staphylococcus epidermidis.
XX
PN WO200134809-A2.
XX
PD 17-MAY-2001.
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PF 09-NOV-2000; 2000WO-US30782.
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PR 09-NOV-1999; 99US-0164258.
XX
PA (GLAXO ) GLAXO GROUP LTD.
XX
PI Kimerly WJ;
XX
DR WPI; 2001-316495/33.
XX
PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
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PT useful for vaccinating against infections, e.g. endocarditis -
XX
PS Claim 8; Page 1427-1428; 2188pp; English.
XX
XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
CC (I) and (II) can have antibacterial activity and therefore can be used
CC in vaccination. The nucleic acids (I) may be used to produce the
CC S. epidermidis polypeptides (II) via the production of vectors
CC containing them which are used to produce hosts cells which express the
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC used to vaccinate subjects and to raise antibodies against the bacteria.
CC The polypeptides may also be used to assay for other inhibitors of their
CC activity and therefore identify compounds that may be used for the
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
CC AAH55090 represent specifically claimed S. epidermidis genomic DNA
CC polynucleotide sequences from the present invention. AAH55091 to
CC AAH55098 represent oligonucleotide sequences and primers which are used
CC in the exemplification of the present invention.
CC N.B. The present invention specifically claims all the polynucleotide
CC sequences given in the sequence listing of the present specification,
CC however the sequence listing only goes up to SEQ ID NO:4454 so even
CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
CC no sequences are present for SEQ ID NO:4455 to 4464.
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SQ Sequence 3825 BP; 1407 A; 526 C; 643 G; 1249 T; 0 other;

Query Match      14.8%; Score 34.6; DB 22; Length 3825;
Best Local Similarity 61.8%; Pred. No. 0.28;
Matches 55; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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DB 720 CTAACTCTGTATTAATCAACCCGAGA 692

RESULT 5
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AC AAS45308;
XX
DT 18-DEC-2001 (first entry)
XX
DE Chemically pretreated genomic DNA associated with cell cycle #7.
XX
KW Cell cycle; human; CpG dinucleotide; cytosine methylation; HIV; aging;
KM human immunodeficiency virus; neurodegenerative disorder; solid tumour;
KM graft-versus-host disease; glomerular disease; lewy body disease; cancer;
KM arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritis;
KM immunosuppressive; antitumour; cytostatic; antiarteriosclerotic; ds;
KM PCR primer.
XX
OS Homo sapiens.
XX
PN WO200168911-A2.
XX
PD 20-SEP-2001.
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PF 15-MAR-2001; 2001WO-EP02945.
XX
PR 15-MAR-2000; 2000DE-1013847.
PR 06-APR-2000; 2000DE-1019058.
PR 07-APR-2000; 2000DE-1019173.
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPiG-) EPIGENOMICS AG.
```


XX PA Olek A, Piepenbrock C, Berlin K;
PI XX
XX PI
DR XX WPI: 2001-602751/68.
XX
PT Designing primers and probes for analysing diseases associated with
PT cytosine methylation state e.g. arthritis, cancer, aging,
PT arteriosclerosis comprising fragments of chemically modified genes
XX associated with cell cycle -
XX
PS Claim 1; SEQ ID No 13; 28pp; English.
XX
CC Sequences AAS4526-AAS4520 represent chemically pretreated genomic DNA
CC molecules associated with the cell cycle and specific PCR primers of the
CC invention. The sequences are useful for detecting the methylation state
CC of all CpG dinucleotides in a sequence and therefore for analysing
CC associated diseases. By analysing cytosine methylations in the pretreated
CC DNA, genetic and/or epigenetic parameters for the diagnosis and therapy
CC of existing diseases or the predisposition to specific diseases can be
CC ascertained. The parameters may be compared to another set of genetic
CC and/or epigenetic parameters, the differences serving as basis for
CC diagnosis and/or prognosis events which are disadvantageous to patients.
CC The sequences of the invention are useful for the diagnosis and therapy
CC of HIV infection, neurodegenerative disorders, graft-versus-host disease,
CC aging, glomerular disease, Lewy body disease, arthritis,
CC arteriosclerosis, solid tumours and cancers.
XX
SQ Sequence 10286 BP; 2629 A; 298 C; 2552 G; 4807 T; 0 other;
XX
Query Match 14.8%; Score 34.4; DB 22; Length 10286;
Best Local Similarity 52.9%; Pred. No. 0.48;
Matches 74; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
XX
OY 2 ttcttcagtttagtaaatgttttagtcctcctatgagtagggtggaagatttgagta 61
DB 1739 ttcttcagtttagtaaatgttttagtcctcctatgagtagggtggaagatttgagta 1798
XX
OY 62 ttgaatgaggaatcctctgagtagtagacttcagaaacaatgactcggaagactacgc 121
DB 1799 ttcttcagtttagtaaatgttttagtcctcctatgagtagggtggaagatttgagta 1858
XX
OY 122 agattattttatttgacatt 141
DB 1859 atgtttgtaattttagtatt 1878
XX
RESULT 6
AAH31486/C
ID AAH31486 standard; cDNA; 621 BP.
XX
AC AAH31486;
XX
DE 30-JUL-2001 (first entry)
XX
DE Human olfactory receptor polynucleotide, SEQ ID NO: 58.
XX
KW Human; olfactory receptor; OR; primary scent determination;
KW secondary scent determination; polypeptide library; odour receptor;
KW scent profile; scent fingerprint; scent representation; ss.
XX
OS Homo sapiens.
XX
PN MO200127158-AZ.
XX
PD 19-APR-2001.
XX
PF 06-OCT-2000; 2000MO-US27582.
XX
PR 08-OCT-1999; 99US-0158615.
XX 24-FEB-2000; 2000US-0184809.
PA (DIGI-) DIGISCENTS.

PA (YEDA) YEDA RES & DEV CO LTD.
XX
XX PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX WPI: 2001-290713/30.
XX
PT New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists -
XX
PS Claim 1; Fig 1; 1857pp; English.
XX
CC The present sequence is one of a number of isolated polynucleotides
CC which encode polypeptides involved in olfactory sensation. The
CC polynucleotides can be used in screening for olfactory agonists and
CC antagonists. The methods allow for the determination of primary
CC scents and the identification of the odour receptors used to detect
CC these primary scents. The methods also enable determination of
CC secondary scents and the identification of combinations of odour
CC receptors that are involved in detecting such secondary scents.
CC This enables the construction of a scent representation (also called
CC a scent fingerprint or scent profile), which may be used to re-create
CC and edit scents. Libraries of olfactory receptors are useful for
CC determining the interaction pattern of a composition with the receptors,
CC and can be used for determining differences in the olfactory faculties
CC of different individuals.
XX
SQ Sequence 621 BP; 212 A; 85 C; 180 G; 136 T; 8 other;
XX
Query Match 13.6%; Score 31.8; DB 22; Length 621;
Best Local Similarity 55.6%; Pred. No. 1.2;
Matches 60; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
XX
OY 53 tttagattttggaatgaggaatcctctgagtagtagacttcagaaacaatgactcgga 112
DB 511 TGTGNAATTCCTCCTTAGAGCTGCTCATACACTGTGACTTCACTAATACATGACATGCCA 452
XX
OY 113 agctaccgagaattattattttgtagctgcctcactacgactaccca 160
DB 451 GGGAATCCACACTGTATGTTCCTAGCCACGAGCTCTTGTGCACCCA 404
XX
RESULT 7
AAH32502/C
ID AAH32502 standard; DNA; 621 BP.
XX
AC AAH32502;
XX
DE 30-JUL-2001 (first entry)
XX
DE Human olfactory receptor polynucleotide, SEQ ID NO: 1075.
XX
KW Human; olfactory receptor; OR; primary scent determination;
KW secondary scent determination; polypeptide library; odour receptor;
KW scent profile; scent fingerprint; scent representation; ds.
XX
OS Homo sapiens.
XX
PN MO200127158-AZ.
XX
PD 19-APR-2001.
XX
PF 06-OCT-2000; 2000MO-US27582.
XX
PR 08-OCT-1999; 99US-0158615.
XX 24-FEB-2000; 2000US-0184809.
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX WPI: 2001-290713/30.
DR

XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW Cytostatic; gene therapy; vaccine; metastasis; ds.
XX Homo sapiens.
OS WO200157182-A2.
XX 09-AUG-2001.
PD 17-JAN-2001; 2001WO-US01354.
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
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PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
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PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 23-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227189.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
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PR 06-SEP-2000; 2000US-0230437.
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PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
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PR 08-SEP-2000; 2000US-0231414.
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PR 12-SEP-2000; 2000US-0232081.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
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PR 21-SEP-2000; 2000US-0234223.
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PR 29-SEP-2000; 2000US-0235837.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
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PR 17-NOV-2000; 2000US-0249265.
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PR 05-DEC-2000; 2000US-0251030.
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 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
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 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 01-DEC-2000; 2000US-0249300.
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 PR 05-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251930.
 PR 05-DEC-2000; 2000US-0251988.
 PR 06-DEC-2000; 2000US-0256719.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251899.
 PR 11-DEC-2000; 2000US-0251990.
 PR 05-JAN-2001; 2001US-0259678.

XX (HUMA-) HUMAN GENOME SCI INC.
 XX

PI Rosen CA, Barash SC, Ruben SM;
 XX

DR WPI; 2001-483426/52.
 XX

PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 useful for preventing, diagnosing and/or treating cancers and

PT metastasis -
 XX
 PS Disclosure; SEQ ID NO 40838; 3071pp + Sequence Listing; English.
 XX

CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
 CC amino acid sequences given in AAM82170 to AAK51921. (I) have cytosolic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/haematopoietic-related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/haematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
 CC represent sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 54877 BP; 15008 A; 10329 C; 11472 G; 18068 T; 0 other;

Query Match 13.3%; Score 31; DB 22; Length 54877;
 Best Local Similarity 52.8%; Pred. No. 13;
 Matches 67; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 16 agaatatgttagtgcctcctatgatagggtggaagattgattgaaatgagcaat 75
 Db 12463 aaattacactgtgctccatcatattctcttggatagtaggcattagaccacatt 12522
 QY 76 ctctgagatgagcttcgaaacacatgactcgcggaagctcgcagattatttatt 135
 Db 12523 ctgagagcttaagacagatgattgaaagacactgagagtaacctattatttatt 12582
 QY 136 ggcattg 142
 Db 12583 gtttttg 12589

RESULT 13
 AAS71803
 ID AAS71803 standard; cDNA; 661 BP.
 XX
 AC AAS71803;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #7607.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR P-PSDB; ABG07616.
 XX

PT New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -

PS Claim 1; SEQ ID No 7607; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at http://wipo.int/pub/published_pat_sequences.

SQ sequence 661 BP; 175 A; 188 C; 97 G; 201 T; 0 other;

Query Match	13.1%	Score 30.6;	DB 23;	Length 661;
Best Local Similarity	56.48;	Pred. No. 3;		
Matches 57; Conservative	0;	Mismatches 44;	Indels 0;	Gaps 0

OY 112 aagctaccgcagatattttatgttgcatgcccacaaagtcataccctcagaftacga 121
| | | | | | | | | | | | | | |
Db 330 aggcacatcgccaatatctctatagaacaatgctcttcaacaacccccagatatacgc 389

OY 172 gatgataagatcalatgtgatgagtcacalcttcacacacgg 212
| | | | | | | | | | | | | | |
Db 390 ccttaccccaanaatcttcttcagtttaactctccacacg 430
| | | | | | | | | | | | | | |

	RESULT	14
AAI97683		
ID	AAI97683	standard; cDNA; 925 BP.

AC AAI97683;

DT 13-NOV-2001 (first entry)

DE	Human neuroblastoma expressed polynucleotide SEQ ID NO 3758.
DE	

KW Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss.

05 Homo sapiens.

PN WO200166719-A1.

PD 13-SEP-2001.

PF 02-MAR-2001; 2001WO-JP01629

PR 07-MAR-2000; 2000JP-0159195

PA (CHIB-) CHIBA PREFECTURE.

(U) UNCLASSIFIED FRANK CO LID
XX XX

PI Nakagawara A;

DR · WPI; 2001-565584/63.

xx Nucleic acids originating in gene expressed in human neuroblastoma,
 pn useful as probe or primer in diagnosing prognosis of human
 pn neuroblastoma, malignancy and susceptibility indicator or tumour marker
 pn for anti-cancer agents -

PS Claim 1; Page 2740; 2979pp; Japanese.

CC The invention relates to novel genes (A1193926-A1197963) expressed in
CC human neuroblastoma. The nucleic acids are applicable as a probe or
CC primer in diagnosing the prognosis of human neuroblastoma, malignancy and
CC susceptibility indicators or tumour markers for anti-cancer agents. The
CC gene information for diagnosing prognosis is related to factors similar
CC to that for N-myc and TrkA genes.

5Q Sequence 925 BP; 273 A; 149 C; 189 G; 287 T; 27 other;

Query Match	13.1%;	Score 30.6;	DB 22;	length 925;
Best Local Similarity	56.4%;	Pred. No. 3.4;		
Matches 57; Conservative	0;	Mismatches 44;	Indels 0;	Gaps 0;

Oy 111 gaagctaccggcgaaggattatattttgcatgtgcctccatcaagtccatccactgaatgagc 170
| | | | | | | | | | | | | | | | | | | | | |
Db 392 gaagcttgaagaagtgatgatgaattttgaacataaaccttcagtaaaagaacaacgaggttg 451

Oy 171 agatgataagaatcacathtgcatgtcgatccatcattccaacac 211
| | | | | | | | | | | | | | | | | | | | | |
Db 452 tagataaaaatgcatgtctcattgacctggtctgtttcttcaatc 492

RESULT	15
ABI99851	
ID	ABI99851 standard; cDNA; 2322 BP.

AC ABT99851;

DT 07-MAR-2002 (first entry)

DE	Mouse	ischaemic condition related	CDNA sequence	SEQ ID NO: 979.

KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;

XX
XX
XX

XX
C

. C N T R O L S C A P I T A L

00000000000000000000
XX XX

ED 22 NOV 77
XX

XX 16-MAY-2001; 2001WC-JF04192.

PR 18-MAY-2000; 2000JP-01459//.
XX

PA (UYNL-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX

PI Ishikawa K, Asai S,
XY

DR WPI; 2002-034733/
DR D-PCDDA APP57340

PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
PT expression levels of particular genes defined in the specification or
PT by determining the expression profile of a gene group comprising these
PT genes -

PS Claim 2; Page 2467-2471; 2690pp; English

The present invention describes a method for examining ischemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischemic condition (e.g. compressive

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 3, 2002, 01:00:35 ; Search time 185.98 Seconds
(without alignments)
307.735 Million cell updates/sec

Title: US-09-300-482-1
Perfect score: 233
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Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.NA.*

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6: /cgn2_6/ptodata/2/1na/Backfilest.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	28.4	12.2	2596	4	US-09-289-254-1 Sequence 1, Appli
C 3	28.4	12.2	17710	4	US-08-976-259-70 Sequence 70, Appli
4	28.2	12.1	12565	4	US-09-345-217-3 Sequence 3, Appli
5	28	12.0	3417	2	US-08-464-402-1 Sequence 1, Appli
6	27.4	11.8	527	4	US-09-054-775C-1 Sequence 1, Appli
7	27.4	11.8	527	4	US-08-976-259-137 Sequence 137, App
8	27.4	11.8	1172	4	US-08-936-165A-8 Sequence 8, Appli
9	27.4	11.8	2442	3	US-09-040-485-1 Sequence 1, Appli
10	27.4	11.8	5892	3	US-08-755-587-27 Sequence 27, Appli
11	27.4	11.8	7240	3	US-08-755-587-15 Sequence 15, Appli
12	27.4	11.8	11283	2	US-08-603-753D-3 Sequence 3, Appli
13	27.4	11.8	11283	4	US-09-099-753-3 Sequence 3, Appli
14	27.4	11.8	11283	4	US-08-986-106-3 Sequence 3, Appli
15	27.4	11.8	11385	2	US-08-639-501-1 Sequence 1, Appli
16	27.4	11.8	11385	3	US-09-044-946-1 Sequence 1, Appli
17	27.4	11.8	11385	3	US-09-044-908-1 Sequence 1, Appli
C 18	27.2	11.7	1153	4	US-08-858-207A-126 Sequence 126, App
C 19	26.6	11.4	3411	4	US-08-146-969-4 Sequence 4, Appli
20	26.6	11.4	4656	4	US-09-425-665-1 Sequence 1, Appli
21	26.6	11.4	4656	4	US-09-685-668-1 Sequence 1, Appli
C 22	26.4	11.3	1791	1	US-08-245-294-7 Sequence 7, Appli
C 23	26.4	11.3	1791	1	US-08-474-499-7 Sequence 7, Appli
C 24	26.4	11.3	1791	1	US-08-307-279A-7 Sequence 7, Appli
C 25	26.4	11.3	1791	5	PCT-US95-06211-7 Sequence 7, Appli
26	26.4	11.3	1917	3	US-08-755-587-1 Sequence 3, Appli
C 27	26.2	11.2	3159	3	US-08-986-485-3 Sequence 3, Appli

C 28	26.2	11.2	11707	4	US-09-136-574A-1 Sequence 1, Appli
C 29	26	11.2	1294	3	US-08-464-523B-3 Sequence 3, Appli
C 30	26	11.2	1553	3	US-08-492-459-21 Sequence 21, Appli
C 31	26	11.2	1553	3	US-08-423-752-21 Sequence 21, Appli
C 32	26	11.2	1553	4	US-08-716-873-35 Sequence 35, Appli
C 33	26	11.2	1553	4	US-09-368-431-35 Sequence 35, Appli
C 34	26	11.2	1553	4	US-09-414-006-21 Sequence 21, Appli
C 35	26	11.2	1776	1	US-08-464-523B-4 Sequence 4, Appli
C 36	26	11.2	2274	3	US-08-492-459-13 Sequence 13, Appli
C 37	26	11.2	2274	3	US-08-423-752-13 Sequence 13, Appli
C 38	26	11.2	2274	4	US-08-716-873-27 Sequence 27, Appli
C 39	26	11.2	2274	4	US-09-368-431-27 Sequence 27, Appli
C 40	26	11.2	2274	4	US-09-414-006-13 Sequence 13, Appli
C 41	25.8	11.1	607	4	US-09-328-111-205 Sequence 205, App
C 42	25.8	11.1	2733	1	US-08-676-967-3 Sequence 3, Appli
C 43	25.8	11.1	2733	1	US-08-676-974-3 Sequence 3, Appli
C 44	25.8	11.1	2733	2	US-09-098-487-3 Sequence 3, Appli
C 45	25.8	11.1	84495	4	US-09-797-906-3 Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-619-554-1/C
Sequence 1, Application US/08619554
Patent No. 5821353
GENERAL INFORMATION:
APPLICANT: DOUGLAS, Cameron M.
APPLICANT: CHREBET, Gary L.
APPLICANT: CLEMAS, Joseph
APPLICANT: EL-SHERBINI, Mohammed
APPLICANT: FOOR, Forrest
APPLICANT: KAHN, Jennifer
APPLICANT: KELLY, Rosemarie, - PARENT, S.A.
APPLICANT: MARRINAN, Jean, - RAMDAN, N.M.
APPLICANT: MORIN, Nancy, - REGISTER, E.A.
APPLICANT: ONISHI, Janet, - SHEL, Gan-du
TITLE OF INVENTION: DNA ENCODING 1,3 BETA-D GLUCAN
TITLE OF INVENTION: SYNTHASE SUBUNIT
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOSEPH A. COPPOLA - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA: US/08/619, 554
APPLICATION NUMBER: US/08/619, 554
FILING DATE: 01-AUG-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COPPOLA, JOSEPH A
REGISTRATION NUMBER: 38, 413
REFERENCE/DOCKET NUMBER: 19104PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-6734
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7655 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-619-554-1

Query Match 12.8%; Score 29.8; DB 1; Length 7655;
Best Local Similarity 54.0%; Pred. No. 1.5;
Matches 61; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 13 agtgaataatgtagtgctcctctgtagtggaagatttgatgatgaagc 72
DB 4310 AGCGAATAGTCTTCTGCTCTCACTTCAGTCAAGGGGCTCTTCATCCAGTAGGCG 4251
QY 73 aatctctgagatgagctcagaacaatgagctcggaagctacccagat 125
DB 4250 AATTGTGAAGTCTGGTAAGCTCTCAGCAACAAACTCAGCATTTTCCAGTTTCAAT 4198

RESULT 2
US-09-289-254-1/c
Sequence 1, Application US/09289254
Patent No. 6299882
GENERAL INFORMATION:
APPLICANT: Junker, David F.
TITLE OF INVENTION: No. 6299882el Recombinant and Mutant Herpesviruses
FILE REFERENCE: SY0994
CURRENT APPLICATION NUMBER: US/09/289,254
CURRENT FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2596
TYPE: DNA
ORGANISM: Marek's Disease Virus 1
US-09-289-254-1

Query Match 12.2%; Score 28.4; DB 4; Length 2596;
Best Local Similarity 58.1%; Pred. No. 2.8;
Matches 50; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 90 ctccagaanaacaatgactcggaagctacccagatattttatgtgcctccat 149
DB 376 CTGTGTAAGTGGGTGACATCGGAATAATGCTGTGATATTGTTGCCATTGCCGTGAC 317
QY 150 cagctcacccatcagatgagatg 175
DB 316 CGTCCGCCGCTTATGTTGGGAATG 291

RESULT 3
US-08-976-259-70/c
Sequence 70, Application US/08976259
Patent No. 6316609
GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Choi, Gail H.
APPLICANT: Welch, Rodney A.
TITLE OF INVENTION: Nucleotide Sequence of Escherichia coli
Patent No. 6316609
NUMBER OF SEQUENCES: 142
CORRESPONDENCE ADDRESS:
ADDRESSER: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,259
FILING DATE: Herewith
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,626 AND US 60/061,953
ATTORNEY/AGENT INFORMATION:
NAME: Scieffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488, 0740002/EKS/CBM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 17710 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-976-259-70

Query Match 12.2%; Score 28.4; DB 4; Length 17710;
Best Local Similarity 50.7%; Pred. No. 6.6;
Matches 68; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 100 catgactcggaagctacccagatattttatgtgcattgcctccatgctacc 159
DB 12783 CGAAGACGAGATMACCTGGCGGCATTTTGTGATGTTGATTCAGCCGCCCTCC 12724
QY 160 atcagatcgagatgataatgcatatgcatgagctcagctccttcacacaccggttgac 219
DB 12723 GACCATCTGACCGCTGACACATTTTCAGACTCCGACACACTTCTGACCGGTTGAC 12664
QY 220 aagggtattgtgtg 233
DB 12663 GATGTTCCGTTG 12650

RESULT 4
US-09-345-217-3
Sequence 3, Application US/09345217
Patent No. 6268142
GENERAL INFORMATION:
APPLICANT: DUFF, GORDON W.
APPLICANT: COX, ANGELA
APPLICANT: CAMP, NICOLA J.
APPLICANT: DIGIOVINE, FRANCESCO S.
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR DISEASES ASSOCIATED
WITH AN IL-1 INFLAMMATORY HAPLOTYPE
FILE REFERENCE: MSA-010, 02
CURRENT APPLICATION NUMBER: US/09/345,217
EARLIER FILING DATE: 1999-06-30
EARLIER APPLICATION NUMBER: PCT/GB98/01481
EARLIER FILING DATE: 1998-05-21
EARLIER APPLICATION NUMBER: 9711040.7
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 12565
TYPE: DNA
ORGANISM: Homo sapiens
US-09-345-217-3

Query Match 12.1%; Score 28.2; DB 4; Length 12565;
Best Local Similarity 53.1%; Pred. No. 6.6;
Matches 60; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 85 tgaagactcagaanaaatgactcggaagctacccagatattttatgtgcattgac 144
DB 12129 tgcctctgacatgtagagctctgcacttgagactgtatgaaagatgctgtgc 12188


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COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,259
FILING DATE: Herewith
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488-0740002/EKS/CBM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
LENGTH: 527 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-976-259-137
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```
Query Match      11.8%; Score 27.4; DB 4; Length 527;
Best Local Similarity 50.8%; Pred. No. 3.1;
Matches 64; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 108 cgggaagctacgcagatatttatttgcatctcctccatcagttcattcagat 167
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 310 CAGATACTGCGCGCATTTTGTGTGATGGTGGATTCAGCGCTCCGCCACCATCT 251

QY 168 gcgagatgataagatcattatgtcagtcagtcacatcttcacacccggttgacaaggta 227
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 250 GACCGTGACACATTTTCAGACTCCGACCCAMCTTCTGCAACGGTGTGACGATGGTTN 191

QY 228 ttgttg 233
    | | | |
Db 190 CGGTTG 185
```

```
RESULT 8
US-08-936-165A-8
; Sequence 8, Application US/08936165A
; Patent No. 6348582
; GENERAL INFORMATION:
; APPLICANT: Black, Michael
; APPLICANT: Burnham, Martin
; APPLICANT: Hodgson, John
; APPLICANT: Knowles, David
; APPLICANT: Lonetto, Michael
; APPLICANT: Nicholas, Richard
; APPLICANT: Pratt, Julie
; APPLICANT: Reichard, Richard
; APPLICANT: Rosenberg, Martin
; APPLICANT: Ward, Judith
; TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides,
; TITLE OF INVENTION: Polypeptides and Their Uses
; NUMBER OF SEQUENCES: 534
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
```

```
APPLICATION NUMBER: US/08/936,165A
FILING DATE: 24-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/027,032
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R.
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50549
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1172 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-08-936-165A-8
```

```
Query Match      11.8%; Score 27.4; DB 4; Length 1172;
Best Local Similarity 55.9%; Pred. No. 4.4;
Matches 52; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 49 aggatttggtattgaatgaagcaatctctgagatagagacttcagaanaaatgactc 108
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 605 AGGAAGTGCTTATGCAATAATTAAGAAAGATATTGTAATAAAGTAAAGAAAGTAAAGCGGCT 664

QY 109 gggaaagctacgcagatatttatttgcatc 141
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 665 GATCCAGTCCCGAAGATTACTAAATAGAGATT 697
```

```
RESULT 9
US-09-040-485-1
; Sequence 1, Application US/09040485
; Patent No. 6166176
; GENERAL INFORMATION:
; APPLICANT: Radosevich, James A.
; TITLE OF INVENTION: A GENE ENCODING A NOVEL MARKER FOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BRINKS, HOFER, GILSON & LYONE
; STREET: NBC Tower - Suite 3600, 455 N. Cityfront
; STREET: Plaza Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60611-5599
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/040,485
; FILING DATE: 17-MAR-1998
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Martin, Alice O.
; REGISTRATION NUMBER: 35,601
; REFERENCE/DOCKET NUMBER: 8998/3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-321-4200
; TELEFAX: 312-321-4299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2442 base pairs
```

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 70..834
US-09-040-485-1

Query Match 11.8%; Score 27.4; DB 4; Length 2442;
Best Local Similarity 55.9%; Pred. No. 6.1;
Matches 52; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 12 tagtagaataatgttagctgcctcctatgataaggtggaagattgagttatgaaatgag 71
||||| ||| || ||||| ||| ||| |||||
DB 620 TAGTAGAAGATGAAAGATTGCACCATGATACATGATGTAACATGCCAAGTCTATGAGG 679
QY 72 caatctctgagatagagacttcagaaacaatg 104
| | | | | | | | | | | | | | | |
DB 680 AACACAGCACTATATGAACTCTAGAAAATGAG 712

RESULT 10
US-08-755-587-27
Sequence 27, Application US/08755587
Patent No. 6045997
GENERAL INFORMATION:
APPLICANT: Futreal, Phillip A
APPLICANT: Wooster, Richard F
APPLICANT: Ashworth, Alan
APPLICANT: Stratton, Michael R
TITLE OF INVENTION: Materials and methods relating to the
TITLE OF INVENTION: Identification and sequencing of the BRCA2 cancer
NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell Seltzer Park & Gibson
STREET: 310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
CITY: Raleigh
STATE: NC
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/755,587
FILING DATE: 25-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9523959.6
FILING DATE: 23-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525555.0
FILING DATE: 14-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9617961.9
FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kenneth D Sibley
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405-135
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 5892 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 483..5412

FEATURE:
NAME/KEY: exon
LOCATION: 481..5412
US-08-755-587-27

Query Match 11.8%; Score 27.4; DB 3; Length 5892;
Best Local Similarity 65.6%; Pred. No. 9;
Matches 40; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 48 aagattgaattgtaagagcaatctctgagatgagacttcagaaacaatgact 107
||||| ||||| ||||| ||| ||| ||||| |||||
DB 4954 AAGATTGAATTGTAAGAACTTAAGTTGAGAGGTGTTCTTCGAAAATAATCACT 5013
QY 108 C 108
|
DB 5014 C 5014

RESULT 11
US-08-755-587-15
Sequence 15, Application US/08755587
Patent No. 6045997
GENERAL INFORMATION:
APPLICANT: Futreal, Phillip A
APPLICANT: Wooster, Richard F
APPLICANT: Ashworth, Alan
APPLICANT: Stratton, Michael R
TITLE OF INVENTION: Materials and methods relating to the
TITLE OF INVENTION: Identification and sequencing of the BRCA2 cancer
NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell Seltzer Park & Gibson
STREET: 310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
CITY: Raleigh
STATE: NC
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/755,587
FILING DATE: 25-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9523959.6
FILING DATE: 23-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525555.0
FILING DATE: 14-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9617961.9
FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kenneth D Sibley
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405-135
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 7240 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-755-587-15

Query Match 11.8%; Score 27.4; DB 3; Length 7240;
Best Local Similarity 65.6%; Pred. No. 9.8;
Matches 40; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

FILING DATE: 17 JAN 1995
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 11283
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo sapiens sapiens
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: adult
TISSUE TYPE: female breast
CELL TYPE: normal and cancerous breast cells
CELL LINE: MCF-7
ORGANELLE: no
IMMEDIATE SOURCE:
LIBRARY: cDNA library derived from human
CLONE: obtained using published sequence
POSITION IN GENOME:
CHROMOSOME/SEGMENT: unknown
MAP POSITION: unknown
UNITS: unknown
FEATURE:
NAME/KEY: BRCA2
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: gene encoding BRCA2 protein
PUBLICATION INFORMATION:
AUTHORS: Wooster, R. et al.
TITLE: Identification of the breast cancer
JOURNAL: Nature
VOLUME: 379
PAGES: 789-792
DATE: 1995
RELEVANT RESIDUES IN SEQ ID NO: 3
US-09-099-753-3

Query Match 11.8%; Score 27.4; DB 3; Length 11283;
Best Local Similarity 65.6%; Pred. No. 12;
Matches 40; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 48 aagcatttgatgtatgaagcgaatctctctgagctatgagacttcaagaacaatgact 107
DB 6579 AAGAAATTTAAATATCAAAATTAAGTGTGAAGGTGTTCTTCAGAAATTAATCACP 6638
QY 108 c 108
DB 6639 C 6639

RESULT 14
US-08-986-106-3
Sequence 3, Application US/08986106
Patent No. 6177410
GENERAL INFORMATION:
APPLICANT: HOLT, JEFFREY T.
APPLICANT: JENSEN, ROY A.
APPLICANT: KING, MARY-CLAIRE
APPLICANT: STEINER, MITCHELL S.
APPLICANT: ROBINSON-BENION, CHERYL L.

APPLICANT: THOMPSON, MARILYN E.
TITLE OF INVENTION: THERAPEUTIC METHODS FOR
PROSTATE CANCER
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARLES A. TAYLOR, JR.
STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER
STREET: BOULEVARD
CITY: DURHAM
STATE: NORTH CAROLINA
COUNTRY: USA
ZIP: 27707
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage
COMPUTER: IBM PC/XT/AT compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORD PERFECT 6.1 and ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,106
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/603,753
FILING DATE: 20 FEB 1996
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 11283
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: BRCA2
PUBLICATION INFORMATION:
AUTHORS: Wooster, R. et al.
TITLE: Identification of the breast cancer
JOURNAL: Nature
VOLUME: 379
PAGES: 789-792
DATE: 1995
US-08-986-106-3

Query Match 11.8%; Score 27.4; DB 4; Length 11283;
Best Local Similarity 65.6%; Pred. No. 12;
Matches 40; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 48 aagcatttgatgtatgaagcgaatctctctgagctatgagacttcaagaacaatgact 107
DB 6579 AAGAAATTTAAATATCAAAATTAAGTGTGAAGGTGTTCTTCAGAAATTAATCACP 6638
QY 108 c 108
DB 6639 C 6639

RESULT 15
US-08-639-501-1
Sequence 1, Application US/08639501
Patent No. 5837492
GENERAL INFORMATION:
APPLICANT: TAVLIGIAN, SEAN V.
APPLICANT: KAMB, ALEXANDER
APPLICANT: SIMARD, JACQUES
APPLICANT: COUCH, FERGUS
APPLICANT: KOMMENS, JOHANNA

```

1 APPLICANT: Weber, Barbara
2 TITLE OF INVENTION: Chromosome 13-Linked Breast Cancer
3 TITLE OF INVENTION: Susceptibility Gene
4 NUMBER OF SEQUENCES: 124
5 CORRESPONDENCE ADDRESS:
6 ADDRESSEE: Venable, Baetjer, Howard & Civiletti
7 STREET: 1201 New York Avenue N.W., Suite 1001
8 CITY: Washington
9 STATE: DC
10 COUNTRY: USA
11 ZIP: 22204
12
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: PatentIn Release #1.0, Version #1.30
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/08/639,501
20 FILING DATE: 29-APR-1996
21 CLASSIFICATION: 530
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: US 08/585,391
24 FILING DATE: 11-JAN-1996
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: US 08/576,559
27 FILING DATE: 21-DEC-1995
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: US 08/575,359
30 FILING DATE: 20-DEC-1995
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: US 08/573,779
33 FILING DATE: 18-DEC-1995
34 ATTORNEY/AGENT INFORMATION:
35 NAME: Ihnen, Jeffrey L.
36 REGISTRATION NUMBER: 28,957
37 REFERENCE/DOCKET NUMBER: 24884-116802-04
38 TELECOMMUNICATION INFORMATION:
39 TELEPHONE: 202-962-4810
40 TELEFAX: 202-962-8300
41 INFORMATION FOR SEQ ID NO: 1:
42 SEQUENCE CHARACTERISTICS:
43 LENGTH: 11385 base pairs
44 TYPE: nucleic acid
45 STRANDEDNESS: single
46 TOPOLOGY: linear
47 MOLECULE TYPE: cDNA
48 HYPOTHETICAL: NO
49 ANTI-SENSE: NO
50 ORIGINAL SOURCE:
51 ORGANISM: Homo sapiens
52 FEATURE:
53 NAME/KEY: CDS
54 LOCATION: 229..10482
55
56 US-08-639-501-1

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					Gaps	0:
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OY	108	c	108			
Dd	6671	C	6671			

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Search completed: July 3, 2002, 07:40:58
Job*time: 24023 sec
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TITLE
JOURNAL

Altafi, H., Nguyen, M., Lam, B., Southwick, A., Ecker, J., Theologidis, A. and Davis, R. W.
Direct Submission
Submitted (26-JUL-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA

COMMENT

On Jun 3, 1998 this sequence version replaced gi:2829860.
Bases 94718-95865 of clone F14J9 overlap with bases 1-1148 of 'IGF'
clone F21M12, gb|AC000132
e-mail for correspondence: arabes@sequence.stanford.edu
Genes with similarity to proteins in the databases are described as
'putative', '-like' or 'similar to'. Genes that have EST
similarity but no significant protein similarity are described as
'unknown proteins'. Genes that are annotated based only on gene
prediction software are described as 'hypothetical proteins'.
The software programs used to predict genes include: Graal
(Informatics Group, Oak Ridge National Laboratory,
http://combio.ornl.gov/section/index.html), GENSCAN (Chris Burge,
http://genomic.stanford.edu/~chris/GENSCANW.html), Rexa (V.Solovay
& A.Selamov, Sanger Centre, http://genomic.sanger.ac.uk/), and
NetPlantene (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/NetPlantene.html).

FEATURES
source

1. 95865

/organism="Arabidopsis thaliana"

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/clone="F14J9"

/note="contains phyA molecular marker"

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/note="Similar to rice water stress induced protein

gi1537404"

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DKYTPSEIGPKPPPLTFNAGMEVPEPSLPTYNLETLKVPPTPRAEDDFLWYTK
DIKPLPPVNLVLAHLRHPENLEAKVAHYCAGAKPWRFTGOEGRNERRDIM
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6504..7028

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/note="Hypothetical protein"

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SLIKLNTFPPASKEITMYTVAEERFAANTYFFISTLRNAGDERDIOACAEAA
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LISEOIVSHWSS"

complement(7954..10925)

/gene="F14J9.4"

complement(7954..8155,8251..8402,8490..8648,

8762..9014,9101..9217,9294..9356,9577..9606,9895..9938,
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/note="Similar to MEN21, gi12598575, Megicaco truncatula

nodulation induced gene"

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FYHHTTIGISKTHMAVAMVITHTGSSGNFLEPPLIIMAAWMAAEIOTKM
SETRAAPYTSLLKMGSLDCCGALISDITSDMSLSPLRISLRYAGVASALA
FCLMSWAMQRKGPLYVSFPLLIIVVAITSWALEKLTHTGTWGSALVIGLTVL
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12867..15018

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join(12867..13122,13720..13911,13990..14156,14269..14533,

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/note="Similar to nodulins and lipase; location of EST

E6C277, gb|AA042309.. similar to nodulins gi13328240,

gi12129854 and others and lipase, gi12129636"

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NSDVGAVAGISYIGLPNGKSPFORSTGRSDRLIDFICOLINTSLNPLYDSLV
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GFRNALYMIIDGONDIDSPSKGSYSRYVKKILINVSSEIKAKITLYDEGRFVW
NTPGLCPQKQKSNVSHSGFEDKHCGLTAYNAALFNEGDLHMGCDRLTEKENTY
VDIYAIRYDILANSNNYGFEPKMACCGGPPYVNVNITCGNGSKSCDEGSRFIS
WDGIHYETANAIVAMKVLMSQHSPTPTPFHFCG"

complement(15279..16596)

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complement(join(15279..15796,15879..16037,16122..16252,

16328..16468,16571..16596)

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/note="Similar to 12-oxophytodienoate reductase,

gi12765083 and old-yellow-enzyme homolog, gi12232254"

/codon_start=1

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/db_xref="GI:3482915"

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GARGYLIDQPKMSDNDRTDSYSGSLNRCGRFALQYEAQSEKGPDRVGRISPPAD
YMESGDTDPKRLGLYMAKSLNREITLCHMIEPRMKYSEIFECRESILTPRNAFNGT
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17046..19163

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17046..19163

/gene="F14J9.7"

/note="Hypothetical protein: Similar to Arabidopsis
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and several others"

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VDDARKTFDVPKETEVSWSMLMGYQNGRIEAEELFSEVPKPIYACNAMSIG
QKGEIARARVFDSEKERNDSWQTVIKIHERNFELEALDPLTLMOKQGRPTFPL
ISLISVCAASLASLHGRQVHAQLVRCQPDVYVAASVLMYTKCGELVSKLFLDFE
PSKDIIMWNSLISGYSASHGDEALKYFCEPMLSGSTKPREVEFVATLSACSYAGME
EGAKIYSMESVVEGPKPIITAHYACVMLGRAGFENAMEIDGMEVPEPAVWGSLL
GACRTHSOLDVAEFCARKLITEIPBNSGYTILSNMYASOGRAVDVLEKIMKTRIV
RKSFGCSWTEYENKVAHFTFGGINSHPQESILKIDLEDLGLREAGYNPDSCIALND
VDEEKVNSLKHSERLAVAYVALTKISEGPIRVMKRLKVCSDCHTAKIKITSKERE
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CDS       /gene="F14J9.8"
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          22252..22346,22444..22691,22778..22982,23217..23318))
          /gene="F14J9.8"
          /note="Similar to glucose-6-phosphate dehydrogenases,
          g112276344, g112829880, g112352919 and others; Location of

Query Match      29.0%; Score 76.2; DB 8; Length 95865;
Best Local Similarity 67.1%; Pred. No.3.4e-10;
Matches 108; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 gaagcaatttgatgattgctgcatgcttcgcaagcagtcgcacagaccagaagagatcg 60
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DB 21876 GAAGCTGTGGATGTGATGTCATGACACATTTGAGATAACGCTCAGGACACAGAGCTGG 21817
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QY 61 aatgcataatattgagaagcatttgcttgatgacattcttcacatagcctgaca 120
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DB 21816 ACTCGAATTAATAGTGAAGAACCTTTTGGTTTAACTCACATTCGTCATCAGTTAAC 21757
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QY 121 caatatctcttcaacttcaggaagaaacaataatag 161
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 21756 AAGTCACCTCTCTCTAAGTTGAAGAGAAACAATCTACAG 21716
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RESULT 3
LOCUS      STG6PDHPI 2058 bp mRNA linear PLN 15-FEB-1996
DEFINITION 5.tuberosum mRNA for glucose-6-phosphate dehydrogenase.
ACCESSION  X83923
VERSION     X83923.1 GI:1197384
KEYWORDS    g6pdh gene; glucose-6-phosphate dehydrogenase.
SOURCE      potato.
ORGANISM    Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; easteris I; Solanales; Solanaceae; Solanum.
REFERENCE   1 (bases 1 to 2058)
AUTHORS     von Schaewen,A., Langenkanper,G., Graeve,K., Wenderoth,I. and
            Scheibe,R.
            Molecular characterization of the plastidic glucose-6-phosphate
            dehydrogenase from potato in comparison to its cytosolic
            counterpart
            Plant Physiol. 109 (4), 1327-1335 (1995)
            96106196
            2 (bases 1 to 2058)
            von Schaewen,A.
            Direct Submission
            Submitted (13-JAN-1995) A. Von Schaewen, Universitaet Osnabrueck,
            FB5 Biologie/Chemie, Pflanzenphysiologie, Barbarastrasse 11, 49076
            Osnabrueck, FRG

FEATURES
source      Location/Qualifiers
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CDS

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AMETPVSLDEIDINEKVRKYLRSKRPQLQLEDVYLGQYKGSNCAKSPAYTDDPTVFN
GSTPTESSAALFIDNARMDGVPELMAGKALHTKRAEIVORRHVGNLYKKNFGND
MDKATNELVIRLOPDEAIVLKLNNKVGGLMRIDRSPDLNLYKAKYRGETPDVYERLL
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NVRNGDLSGSD"

BASE COUNT      606 a      372 c      454 g      626 t
ORIGIN

Query Match      26.1%; Score 68.6; DB 8; Length 2058;
Best Local Similarity 52.8%; Pred. No. 4.2e-08;
Matches 131; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

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DB 667 ATTCGTGATGTGTGGCATGTGCAGTCTTAAAGCTCTTCAACAAGTGGTGACAAG 726
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QY 66 cataatattgagaagcatttgcttgatgacattcttcacatagcctgacacata 125
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DB 727 GGTCAATTGTGAGAACCATTTGGTCGATTTTGAAATCATCTAGTACGCTGACACAGATC 786
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QY 126 tctcttcaaaccttcaggaagaaacaataatagaaatlgancatcactaagaagaa 185
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DB 787 CCTAAGAGTACTACTGAGGAGCAAAATTTCCGAATGACCATTACTTGGGAAGA 846
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QY 186 tcncagtnaaatctcctcaggttaaggggttcaaanngntttgaagcaactttag 245
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DB 847 ACTTGTTGAGAACTCTCAGTTCGTTCCGAATCTGTCTTTGAGGCTCTTGGTC 906
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QY 246 ngnagant 253
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DB 907 CAGAAACT 914

RESULT 4
LOCUS      SC000184 1396 bp mRNA linear PLN 23-JUL-1997
DEFINITION Spinacia oleracea mRNA for glucose-6-phosphate dehydrogenase,
            partial, clone 028FA38.
ACCESSION  AF000184
VERSION     AF000184.1 GI:2276347
KEYWORDS    G6PD gene; glucose-6-phosphate dehydrogenase.
SOURCE      Spinach.
ORGANISM    Spinacia oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
REFERENCE   1 (bases 1 to 1396)
AUTHORS     Fink,A.
            Direct Submission
            Submitted (21-JUL-1997) Fink A., Laboratoire de Biochimie et de
            Physiologie Vegetale, University of Geneva, 3, Place de
            l'Universite, CH-1211 Geneva 4, SWITZERLAND
            2 (bases 1 to 1396)
            Fink,A., Diogon,T., Perroud,P.F., Crespi,P. and Greppin,H.
            Nucleotide sequences of glucose-6-phosphate dehydrogenase from
            Spinacia oleracea cloned by RT-PCR
            Unpublished

FEATURES
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gene
CDS

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SIPINIFVDVAVRCVSHRASSASGWTIRVYKPGPGRDSSRELTSRQKQLSDQIFR
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BASE COUNT      418 a      252 c      329 g      397 t
ORIGIN

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Query Match	25.3%	Score 66.6:	DB 8:	Length 1396:
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			Gaps	0:
Oy	8	tttttgatgctgcgtcatgctcttgaaagcagtgctcagaccaggaagatgaaatcgca	67	
Db	500	TTGTGTGAGTGTGGTGAAGATGCTGTAGCCATTCGACGCTTCTTCGCAAGTGGATGGACAAAGG	559	
Oy	68	taataattgagaagcatttggtcttgatgcatcttcccatagagctgcacaataatc	127	
Db	560	TTATAGTGTGAAAGAGCCTTTGTGAGTGCATCGAATTTCTTCGTGACCTACTAGAAAGCT	619	
Oy	128	ttcttcaacttccagaaagaacaataatagatgancatctactagaagaatc	187	
Db	620	TCACACCACTACTTGTAGCGAGACCGACGATTTTCAGATGATGACCATTAATCTTGGGGAAGGAGT	679	
Oy	188	ncagtaaatatcccttcaggtcttaaggggtccaaannagntcttgagccacttngagn	247	
Db	680	TGGTGTGAATATTTATCTTCTACCGCTTTTCAAAATCTATGTTTGAACCTTATGGTCAA	739	
Oy	248	gnaent	253	
Db	740	GGAAGT	745	
RESULT	5			
LOCUS	S0000182	2049 bp	mRNA	linear
DEFINITION	Spinacia oleracea mRNA for glucose-6-phosphate dehydrogenase, clones 028FA14 & 030A4.			
ACCESSION	AJ0000182			
VERSION	AJ0000182.1	GI:2276343		
KEYWORDS	g6pd gene; glucose-6-phosphate dehydrogenase.			
SOURCE	Spinach.			
ORGANISM	Spinacia oleracea			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Caryophyllales; Chenopodiales; Spinacia.			
REFERENCE	1 (bases 1 to 2049)			
AUTHORS	Fink, A.			
TITLE	Direct Submission			
JOURNAL	Submitted (21-JUL-1997) Fink A., Laboratoire de Biochimie et de Physiologie Vegetale, University of Geneva, 3, Place de l'Universite, CH-1211 Geneve 4, SWITZERLAND			
REFERENCE	2 (bases 1 to 2049)			
AUTHORS	Fink, A., Diopon, T., Perroud, P. F., Crespi, P. and Greppin, H.			
TITLE	Nucleotide sequences of glucose-6-phosphate dehydrogenase from Spinacia oleracea cloned by RT-PCR			
JOURNAL	Unpublished			
FEATURES	Location/Qualifiers			
SOURCE	1..2049			

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misc_feature	922. .942 /gene="G6pd" /function="G6pd catalytic site" 1660. .2049 /organism="Spinacia oleracea" /plasmid="pZ11" /cultivar="Matador" /db_xref="taxon:3562" /clone="O30A4" /tissue_type="leaves" /dev_stage="vegetative" 2028. .2036 /gene="G6pd" 2049 /gene="G6pd"		
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ORIGIN	614 t		

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Best Local	Similarity	52.4%	Pred.	Mismatches	117	Indels	0	Gaps
Matches	129	Conservative	0	Matches	117	Indels	0	Gaps
Qy	8	ttttggaatglttcgcatgctcttgcaaacgagltgcaccagaccagaagatgaaatcgca	67					
Db	763	TTGTGGATGTGTGATGATGTGTACCCATCGACGTTCTTCTCAAGTGGATGGACAAGG	822					
Qy	68	taattttgaagaagccatttgctcttgaaagacttctccatagctgcgaacaatc	127					
Db	823	TTATAGTGGAAAGGCTTTTGGACGTGACTCGGATTTCTTCTGTACCTAACTAGAGCT	882					
Qy	128	ttcttccaacttccaagaaagcaaatatataagaaatgancatcactaggaagaaac	187					
Db	883	TCAACGACTACTTGGACGCGAGCAGATATTCAGGATTCACCTATCTTGGGGAAGGAGT	942					
Qy	188	ncagtnaaactcccaagttttaaaggtttcaaanmnanttttgaagcaactltagann	247					
Db	943	TGTGTGAGATTTATCTGTCTTACGCTTTTCAAACTAGTTTTTAACCTCTATGGTCAA	1002					
Qy	248	gaacnt	253					
Db	1003	GGAAGCT	1008					

RESULT	6	580 bp	mRNA	linear	PLN 17-OCT-2000
LOCUS	AF260736				
DEFINITION	Cucurbita pepo plastidic glucose-6-phosphate dehydrogenase mRNA,				
ACCESSION	AF260736				
VERSION	AF260736.1	GI:10834743			
KEYWORDS					
SOURCE	Cucurbita pepo.				
ORGANISM	Cucurbita pepo				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.				
AUTHORS	1 (bases 1 to 580)				
TITLE	Havelda,Z. and Maule,A.J.				
JOURNAL	Complex spatial responses to cucumber mosaic virus replication in susceptible Cucurbita pepo L. cotyledons				
REFERENCE	Plant Cell (2000) In press				
AUTHORS	2 (bases 1 to 580)				
TITLE	Havelda,Z. and Maule,A.J.				
JOURNAL	Direct Submission				
FEATURES	Submitted (26-Apr-2000) Department of Virus, John Innes Centre, Colney Lane, Norwich, Norfolk NR4 7UH, UK				
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BASE COUNT	155 a	150 g	158 t		
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Best Local Similarity	55.9%;	Pred. No. 3.6e-07;			
Matches 109;	Conservative 0;	Mismatches 86;	Indels 0;	Gaps 0;	
OY	59 ggaatcgatataatttagaagcatttgcttgatgcacttctccatagactga	118			
DB	1 GGACACGGGTTATGTTGTAAGAGCCATTGGCCGGATCTCGATCTTCGGGTAGCTAA	60			
OY	119 cacaatattcttctcaactctcagaaagcaaatatagatgancactactag	178			
DB	61 CGAGAGGCTTAAAGAAATATCTCACAGANAGCAAAATTTAGAGTTGATCATTTATTGG	120			
OY	179 gaaggaatcncagthaatatctcncaggttaaggggttcaaanmagnttlyagccac	238			
DB	121 GCAMGAGCTCTGTAGAGAACTGTCGGTTCCTGCATTCTCCAACTCTGTTTGGAGCCTC	180			
OY	239 cttinganmagnt 253				
DB	181 TTTGGTCGAGAGGCT 195				
RESULT	7				
LOCUS	NTTPG18	1869 bp	mRNA	linear	PLN 17-AUG-1999
DEFINITION	Nicotiana tabacum mRNA for plastidic glucose-6-phosphate				
ACCESSION	dehydrogenase TPG18.				
VERSION	AJ001772				
KEYWORDS	AJ001772.1 GI:3021531				
SOURCE	glucose-6-phosphate dehydrogenase.				
	common tobacco.				

REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
ORGANISM	Nicotiana tabacum	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; easterids I; Solanales; Solanaceae; Nicotiana.		
1 (bases 1 to 1869)	Wendt, U. K., Hauschild, R., Lange, C., Pietersma, M., Wenderoth, I. and von Schawen, A.	Evidence for functional convergence of redox regulation in G6PDH isoforms of cyanobacteria and higher plants	Plant Mol. Biol. 40 (3), 487-494 (1999)	
2 (bases 1 to 1869)	von Schawen, A.	Direct Submission	Submitted (18-SEP-1997) von Schawen A., Plant Physiology, University Osnabrueck, Barbarastr. 11, D-49069 Osnabrueck, GERMANY	
JOURNAL	Location/Qualifiers			
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22. 1788	/note="TCG18"			
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BASE COUNT	556 a	342 c	433 g	538 t
ORIGIN				
Query Match	23.7%	Score 62.2;	DB 8;	Length 1869;
Best Local Similarity	51.2%;	Pred. No. 2,1e-06;		
Matches 127; Conservative	0;	Mismatches 121;	Indels 0;	Gaps 0;
QY	6	actttgagatgttcgcgtcaatcttcgcaagcagctgcacgaccagaaggaatggaatcg	65	
DB	681	ATTTCGGATGATGGGATGTGCAAGCTTAAGCTTCAACAAGTGGGTGACAAAG	740	
QY	66	caataatttggaagccatttgcttgatgacacttcctccataggctgacaata	125	
DB	741	AGTCATGTGTGAGAAACCGTTTGGTCGGACTTAATAATCATCTAGTGCTGACCAAGATG	800	
QY	126	tcttcttcaaaccttcagaaagacaatatagaattgncactcaactaggaagaa	185	
DB	801	CCTAAGAAGATCTCACTACGAGGACCAATATATCCGATTTGACCTTACTTGGGAAAGCA	860	
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DB	861	ACTGTGTGAGATCTCTCAGTCTTGCTTTCGCAATCTTGCTTGGACCTCTCTGTC	920	
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LOCUS U32737 10195 bp DNA linear BCT 29-MAY-1998
DEFINITION Haemophilus influenzae Rd section 52 of 163 of the complete genome.
ACCESSION U32737 LA2023
VERSION U32737.1 GI:1573536
KEYWORDS
SOURCE Haemophilus influenzae Rd.
ORGANISM Haemophilus influenzae Rd
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
REFERENCE 1 (bases 1 to 10195)
AUTHORS Fleischmann,R.D., Adams,M.D., White,O., Clayton,R.A.,
Kirkness,E.F., Kerlavage,A.R., Bult,C.J., Tomb,J., Dougherty,B.A.,
Merrick,M., McKenney,K., Sutton,G., FitzHugh,W., Fields,C.A.,
Goodyear,J.D., Scott,J.D., Shiley,R., Liu,L.I., Glodek,A.,
Kelley,J.M., Weidman,J.F., Phillips,C.A., Spriggs,T., Hedblom,E.,
Cotton,M.D., Uterback,T., Hanna,M.C., Nguyen,D.T., Saudek,D.M.,
Brandon,R.C., Fine,L.D., Frichman,J.L., Fuhrmann,J.L.,
Georgagen,N.S., Gnehm,C.L., McDonald,L.A., Small,K.V., Fraser,C.M.,
Smith,H.O. and Venter,J.C.
TITLE Whole-genome random sequencing and assembly of Haemophilus
influenzae Rd
JOURNAL Science 269 (5223), 496-512 (1995)
MEDLINE 95350630
REFERENCE 2 (bases 1 to 10195)
AUTHORS Tatusov,R.L., Mshagiani,A.R., Bork,P., Brown,N.P., Hayes,W.S.,
Borodovsky,M., Rudd,K.E. and Koonin,E.V.
TITLE Metabolism and evolution of Haemophilus influenzae deduced from a
whole-genome comparison with Escherichia coli
JOURNAL Curr. Biol. 6 (3), 279-291 (1996)
MEDLINE 96390784
REFERENCE 3 (bases 1 to 10195)
AUTHORS White,O., Clayton,R.A., Kerlavage,A.R. and Fleischmann,R.D.
TITLE Direct Submission
JOURNAL Submitted (25-JUL-1995) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
4 (bases 1 to 10195)
AUTHORS White,O., Clayton,R.A., Kerlavage,A.R. and Fleischmann,R.D.
TITLE Direct Submission
JOURNAL Submitted (27-SEP-1997) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
REMARK The H. influenzae sequence has been updated by R. Fleischmann. New
database matches have been assigned. Product names have been
improved, and a number of frame shifts have been corrected. We
gratefully acknowledge the work of Tatusov et. al. We have
incorporated their annotation into the /notes fields of the
corresponding H. influenzae genes
5 (bases 1 to 10195)
AUTHORS White,O., Clayton,R.A., Kerlavage,A.R., Fleischmann,R.D.,
Peterson,J., Hickey,E., Dodson,R. and Gwinn,M.
TITLE Direct Submission
JOURNAL Submitted (28-MAY-1998) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
REMARK The whole genome was shifted by 588 nucleotides for a new start
On Sep 30, 1996 this sequence version replaced gi:1221227.
COMMENT Location/Qualifiers
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Matches 110; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
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RESULT 9
ATG6PDHES 1630 bp mRNA linear PLN 31-JAN-1996
LOCUS A.thaliana mRNA for glucose-6-phosphate dehydrogenase (clone E5).
DEFINITION X84229
ACCESSION X84229
VERSION X84229.1 GI:1166404
KEYWORDS 960ph gene; glucose-6-phosphate dehydrogenase.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 1630)
Fink,A., Greppin,H. and Tacchini,P.
Nucleotide sequence of a cDNA encoding the glucose-6-phosphate
dehydrogenase from Arabidopsis thaliana
Unpublished
2 (bases 1 to 1630)
Fink,A.F.A.
Direct Submission
Submitted (23-JAN-1995) A.F.A. Fink, Lab de Biochimie et de
Physiologie, Vigintales, Universiti de Geneve, 3 Place de
l'Universiti, 1211 Geneva, SWITZERLAND
FEATURES
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[illegible]

AUTHORS vonSchaewen,A.
TITLE Direct Submission
JOURNAL Submitted (23-SEP-1998) vonSchaewen A., Plant Physiology,
University Osnabrueck, Barbarastr. 11, D-49069 Osnabrueck, GERMANY
COMMENT On Sep 25, 1998 this sequence version replaced gi:3021530.
FEATURES
Location/Qualifiers

source
1. 1942
/organism="Nicotiana tabacum"
/cultivar="Samsun NN"
/db_xref="taxon:4097"
/cell_type="mesophyll"
/tissue_type="Young sink leaves"
41..232
sig_peptide
41..1801
/note="TPG16"
/product="glucose-6-phosphate dehydrogenase"
233..1798
/product="glucose-6-phosphate dehydrogenase"
BASE COUNT 584 a 353 c 442 g 563 t
ORIGIN

Query Match 23.0%; Score 60.6; DB 8; Length 1942;
Best Local Similarity 50.8%; Pred. No. 5.6e-06;
Matches 126; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

QY 6 acttttgagtgctgcgtatcttgcagcagtcctcagaccaggaaggaatgcg 65
DB 694 ACTTCGGATGTGTCGATGTCGAAGCTTTAAAGCTTCTTCAACAAGGGTGGAGCAAG 753
QY 66 cataatattggaagcattgcttgatcagcatttcccatagcctacacata 125
DB 754 AGTCATTGTTGAGAAACCTTTGTCGTCATTGAAATCATCTTAACGACTTACCAAGAAG 813
QY 126 tcttcttcaaaccttcagaaacaaatatagatagatcctactaggaagaa 185
DB 814 CCTAAGAAGTACCTAAGCAGAGCAATATTCGAAATTCACCTTACTTGGAAGAAG 873
QY 186 tccagctaaatcctcncaggtttaagggttcaaanmagnitttgagccacttngag 245
DB 874 ACTTGTTGAGAACTCTCGTCTTCTTCGAAATCTTGTCTTGTAGAGCCTCTGTGTC 933
QY 246 ngnacnt 253
DB 934 CAGAAACT 941

RESULT 12

ATJ00135 1975 bp mRNA linear PLN 17-AUG-1999
LOCUS Arabidopsis thaliana cDNA encoding plastidic glucose-6-phosphate
DEFINITION dehydrogenase.
ACCESSION AF001359
VERSION AF001359.1 GI:3021304
KEYWORDS glucose-6-phosphate dehydrogenase.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana

REFERENCE
1 (bases 1 to 1975)
Wendt,U.K., Haenschild,R., Lange,C., Pieterama,M., Wenderoth,I. and
von Schaewen,A.
Evidance for functional convergence of redox regulation in G6PDH
isoforms of cyanobacteria and higher plants
Plant Mol. Biol. 40 (3), 487-494 (1999)

JOURNAL MEDLINE
99364543
2 (bases 1 to 1975)
AUTHORS von Schaewen,A.
TITLE Direct Submission
JOURNML Submitted (18-SEP-1997) von Schaewen A., Plant Physiology,
University Osnabrueck, Barbarastr. 11, D-49069 Osnabrueck, GERMANY
FEATURES
Location/Qualifiers

source

1. 1975
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/tissue_type="Above ground parts"
71..1801
CDS

BASE COUNT 563 a 382 c 447 g 563 t
ORIGIN

Query Match 22.8%; Score 60; DB 8; Length 1975;
Best Local Similarity 52.5%; Pred. No. 8.1e-06;
Matches 114; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 37 agtgcagaccagaaaggaatggaatgcataatattggaagccattgcttgat 96
DB 728 AGAGCCTCTCAGAGAAAGCGCTGGACAAAGGGTCAATGTGGAAGACCATTTGGCCGTGAC 787
QY 97 gcacttctccatagcctgacacatatcttcaacttcaggaagaacaata 156
DB 788 TCTGAATATCCGGAGACTTAAGTATGATGCTGAAACAGTATCTTACAGAGACCAATC 847
QY 157 tatgaattgancatctactagaaaggaatcncaglnaaatcctcncaggttta 216
DB 848 TTCAGATTGATCACTATTGGAAGGAGCTTGTGGAACCTTTCAGTCTCCGATTC 907
QY 217 tcaaanmagnitttgagccacacttngagngnancnt 253
DB 908 TCAAAATCTTGTTCGAGCCTGTGTGCAAGAAATT 944

RESULT 13

ATG6PDH15 1772 bp mRNA linear PLN 15-AUG-1997
LOCUS A.thaliana mRNA for glucose-6-phosphate dehydrogenase (clone E15).
DEFINITION X84230
ACCESSION X84230
VERSION X84230.1 GI:1174335
KEYWORDS g6pdh gene; glucose-6-phosphate dehydrogenase.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana

REFERENCE
1 (bases 1 to 1772)
Fink,A., Greplin,H. and Tacchini,P.
Nucleotide sequence of a cDNA encoding the glucose-6-phosphate
dehydrogenase (GenBank X84230) from Arabidopsis thaliana
Plant Physiol. 108, 1343-1343 (1995)
Ref [3]: Plant Gene Register PGR95-021 (1995).

JOURNAL MEDLINE
99364543
2 (bases 1 to 1772)
AUTHORS Fink,A., Greplin,H. and Tacchini,P.
TITLE Direct Submission
JOURNML Submitted (23-JAN-1995) A.F.A. Fink, Lab de Biochimie et de
physiologie, vitales, Universiti de Geneve, 3 Place de
l'Universiti, 1211 Geneva, SWITZERLAND
REFERENCE
1 (bases 1 to 1772)
Fink,A., Greplin,H. and Tacchini,P.
Nucleotide sequence of a cDNA encoding the glucose-6-phosphate
dehydrogenase (GenBank X84230) from Arabidopsis thaliana
Plant Physiol. 108, 1343-1343 (1995)
COMMENT Ref [3]: Plant Gene Register PGR95-021 (1995).
FEATURES
1. 1772
Location/Qualifiers
/organism="Arabidopsis thaliana"

BASE COUNT	polya_signal	polya_signal	gene	CDS
526 a	331 c	419 g	496 t	<p> /cultivar="Columbia" /db_xref="taxon:3702" /clone="E15" /haplotype="diploid" /cell_line="Athaliana Co" /tissue_type="leaves, stems, flowers and roots" /clone_1ib="lambda Zap" /dev_stage="adult" 141. .1685 141. .1685 /gene="G6PDH" 141. .1685 /gene="G6PDH" /EC_number="1.1.1.49" /codon_start=1 /product="glucose-6-phosphate 1-dehydrogenase" /protein_id="CA59012.1" /db_xref="GI:1174336" /db_xref="SWISS-PROT:O43727" /translation="MGVATNPASLSDSGDQLTEHHVTKGESTLSITVVGASGDLMKEE IIFPLAFYEGCLPDQSVNPGVARTKLTITHELADMTSSITCTCIDOREKGMKBBR LKRFYHSGOENSEEDPAELNKKLKEKEAGKTSRLRYLSPNIFDVNCASTRSS SEWMTIVAEKPPGRSESSGELTRCLKOYLTEQYLFRIIDYLGKLEVLVLRFS NLVEFPLMSRYINVELIFSEDGTRGQGFPOYGIIRIDIMONHLQIILALAMEFT PVSADADDINSEKVKVLRSMKPLRLLEVVGQYGNKGGKTPAYRDDPVPNHSLSL PTFSAAMFINNARMDGCVPLFMKAGKALHTGAEIRVOFRVFNPLNKKSPATNLDJNNA TNEIIVRQDEGILIRINKKPGILRGRLDSDNLILRSRYPREIIPAYRRLLDIAI EGERRFLIRSDLEDAAMDLTTPALKELEKKIIPELYGSRGPGVGAHYLASKNNVNRK GDCGEA" 1756. .1761 1772 </p>

[illegible]

TITLE	JOURNAL	MEDLINE	REFERENCE	AUTHORS	JOURNAL	COMMENT	FEATURES	source																																				
Charlil, A., Chetouani, F., Couve, E., de Daruvar, A., Deloux, P., Domann, E., Dominguez-Bernal, G., Duchan, E., Durant, L., Dusserget, O., Entian, K.D., Esin, H., Portillo, F.G., Garrido, P., Gautier, L., Goebel, W., Gomez-Lopez, N., Hain, T., Haut, J., Jackson, D., Jones, L.M., Kaerst, U., Kreft, J., Kuhn, M., Kunz, F., Kurapat, G., Madueno, E., Mallow, A., Vicente, J.M., Ng, E., Nedjari, H., Nordstiek, G., Nollau, S., de Pablo, B., Perez-Diaz, J.C., Purcell, R., Rammel, B., Rose, M., Schlucker, T., Simoes, N., Trierer, A., Vazquez-Boland, J.A., Voss, H., Wehland, J. and Cossart, P.	Science	294 (5543), 849-852 (2001)	Comparative genomics of <i>Listeria</i> species	2 (bases 1 to 347050)	Glaser, P., Frangeul, L. and Rusniok, C.	Direct Submission	Submitted (06-JUN-2001)	Glaser P., Institut Pasteur, Genomique des Microorganismes Pathogenes, 25 rue du Docteur Roux, 75724 Paris Cedex 15, FRANCE																																				
E-mail: pglaser@pasteur.fr	Phone: +33 1 45 68 89 96, Fax: +33 (0)1 45 68 87 86.	Location/Qualifiers	1. 347050	/organism="Listeria monocytogenes"	/strain="EGD-e"	/db_xref="taxon:1639"	complement(95. .841)	/gene="lmo1688"	complement(95. .841)	/gene="lmo1688"	/note="similar to glucose 1-dehydrogenase"	/codon_start=1	/transl_table=1	/protein_id="CAC99766.1"	/db_xref="GI:16411142"	/translation="MNKVALVTGSSRGELREIALALAKEGYDIAVNFSSRRKRAEEVQ QEIEQGRKRVIFKANVDYKREYKRELFKANADEFGRLDITINNAASVLEPLMEES HMWMTMINAKALLFEGQAEKLMQRHOSKTIISLSIGSRIDENITTVGSKAWE SLIRYLAPELAPGIAVNAVSGI,IEIDALNHPNREELLKDAVSKTPAGRMIEPDL VNAVLF,FLASEKADIRICOTIILVDGRTILV"	complement(join(845. .1942,1948. .1953))	/gene="lmo1689"	complement(845. .1942)	/gene="lmo1689"	/note="similar to A/G-specific adenine glycosylase"	/codon_start=1	/transl_table=1	/protein_id="CAC99767.1"	/db_xref="GI:16411143"	/translation="MRMKRLTWDETKITAFQEALVSWYEAANKRVLPWRENTPEYRIW VSIIMLOQTQVDVPIVYFNFRPTQFPFMESFVNADADILKAWEGCYASRVNRLQFA MKQVMADSGEVPTDLTTIISLKGVGYPITAGILSTAYNOAEPAVGNVRYARVLE ICGDINKASRKTIEEYITLOLDIKKNPAARNOGMEIGALVCPTRPMCLGLOPQC EARKNGEYTPYPIKIKYKRRKTKELLSIYISDGIATIEKRENGILANMPPTIE ISKKEDEYAKIQFLHNYGLEVLLDEDEPIAHITKHWESHLVWKMDIRVAKQSIAPNEN WYPATEEEMKRIAFPPVQOMQAMKDFGE"	complement(850. .855)	/gene="lmo1688"	complement(850. .855)	/gene="lmo1688"	complement(1948. .1953)	/gene="lmo1689"	join(2129. .3123,3130. .3147)	/gene="lmo1690"	2129. .2134	/gene="lmo1690"	2143. .3123	/gene="lmo1690"	/note="similar to hypothetical proteins"	/codon_start=1	/transl_table=1	/protein_id="CAC99768.1"	/db_xref="GI:16411144"	/translation="MDTGHVHWGIALGALATVPVAVGSSQAIGIMATITIGSQIP

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PI Yamamoto RT, Xu HH;
XX
DR WPI: 2001-611495/70.
XX P-PSDB: AAN35462.
XX
PT New polynucleotides for the identification and development of
XX antibiotics, comprise sequences of antisense nucleic acids -
XX
PS Claim 27: seq ID No 6958; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes themselves and the encoded proteins. The prokaryotes used are
CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence encodes an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1485 BP; 445 A; 274 C; 333 G; 433 T; 0 other;

Query Match 23.3%; Score 61.4; DB 23; Length 1485;
Best Local Similarity 52.1%; Pred. No. 1.8e-08;
Matches 110; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 53 agggatggaatcgcatatatttggaagcatttgcttgagacttcctccata 112
DB 422 atggctggaagaacgtatttcgtgaaaacatttgatgaatgaaaacagycgcaa 481
QY 113 ggcctacacaatattcttccaacttcaggaagaacaatatagaattgancct 172
DB 482 cattagaagctacaatccacgcttcttgaagaacacaattatcgtatcgatcatt 541
QY 173 tactaggaaggaatcncagttnaaaatccctncaggtttaagggttcaaanmagnuttg 232
DB 542 atttggtaagaagaacgcttcaaaactgctcgctattacgttttccaatgttggttg 601
QY 233 agccacctngagmgngnactnnmngana 263
DB 602 aaccgcttggaaccgctaatcattcattgatta 632

RESULT 2
AAC79584
ID AAC79584 standard; DNA; 6132 BP.
XX
AC AAC79584;
XX
DT 08-FEB-2001 (first entry)
XX
DE Virulence gene #4.
XX
XX Virulence gene #4.
XX
KW Virulence gene; antibacterial; vaccine; bacterial infection;
KM septilemia; bronchopneumonia; rhinitis; wound infection; ss.
XX
OS Pasteurella multocida.
XX
PN WO200061724-A2.
XX
PD 19-OCT-2000.
XX

PF 06-APR-2000; 2000WO-US09218.
XX
XX 09-APR-1999; 99US-0128689.
PR 10-SEP-1999; 99US-0153453.
XX
XX (PHNA) PHARMACIA & UPJOHN INC.
XX
PI Lowery DE, Fuller TE, Kennedy MJ;
XX
DR WPI: 2000-647422/62.
XX P-PSDB: AAB44524.
XX
PT Attenuated Pasteurellaceae bacteria comprising mutations in virulence
XX genes, useful as a live attenuated vaccine against bacterial infections
XX
PS Claim 1: Pages 72-76; 322pp; English.
XX
CC The family Pasteurellaceae encompasses several pathogens that infect a
CC wide variety of animals. The present invention relates to virulence genes
CC from Pasteurellaceae. The present sequence is one such virulence gene.
CC The present sequence may be mutated in order to produce an inactive gene.
CC The inactive virulence gene may in turn be used to produce a vaccine,
CC which is useful for treating bacterial infections such as septilemias,
CC bronchopneumonias, rhinitis and wound infections.
XX
SQ Sequence 6132 BP; 1838 A; 1154 C; 1409 G; 1731 T; 0 other;

Query Match 22.7%; Score 59.6; DB 21; Length 6132;
Best Local Similarity 51.4%; Pred. No. 9.6e-08;
Matches 110; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 50 agaaagatggaatcgcatatatttggaagcatttgcttgatgcacttcctccc 109
DB 2903 agtttgctggaagcgggttaatttgtygaaaacggttggttgatatacgacgycgcaa 2962
QY 110 atagcgcgacaatattcttccaacttcaggaagaacaatatagaattganc 169
DB 2963 aagaccctcgatattccaatccacgcttcttgaatgaaacacaattatcgtatcgacc 3022
QY 170 atctactaggaaggaatcncagttnaaaatccctncaggtttaagggttcaaanmagnut 229
DB 3023 actactctgtgtaagaagaacggttcaaaatctgctgttgctgttcttctaagtgatggt 3082
QY 230 ttgagccacctngagmgngnactnnmngana 263
DB 3083 ttgaaccactcgggaaccgcaattcattcattgatta 3116

RESULT 3
AAC34618
ID AAC34618 standard; DNA; 1905 BP.
XX
AC AAC34618;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 7277.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
KW Protein Identification; signal transduction pathway;
KM metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR

PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125758.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
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PR 16-APR-1999; 99US-0128845.
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PR 07-SEP-1999; 99US-0152363.
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PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
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PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156456.
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PR 04-OCT-1999; 99US-0157117.

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PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
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PR 14-OCT-1999; 99US-0159637.
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PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

```

```

Query Match      22.4%; Score 59; DB 21; Length 1905;
Best Local Similarity 50.4%; Pred. No. 1e-07;
Matches 125; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

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```

QY 6 acttggatgttgctgcatactcttcgaagcagctgcagaccgaagagatgcatcg 65
DB 670 attcgttgtgtggttagtgctgaagtccttagagcctcctcagaagaatgctgacaa 729
QY 66 cataatattggaagcattgctgcttgatgacttcttcctccatgaagctacacata 125
DB 730 ggtcattggaagaaagccattgctgctgacccgaatcattcgaagatgactagatg 789
QY 126 tcttcttcaaaccttcgaagaaacaaatataatagaattgacatactactagaagaa 185
DB 790 tctgaacagatctctacagagagcaaatcttcagatgactacactatttggaagaa 849
QY 186 tencaglnaaaatcctncaggtttaagggttcaannmagnttttgacaccttngag 245
DB 850 gcttgttgagaacaccttcagtgctcgcattcctaattcttcttgagaccttgatgc 909
QY 246 mngnaent 253
DB 910 aagaaatt 917

```

```

RESULT 4
AAS52910
ID AAS52910 standard; DNA; 1524 BP.
XX AAS52910;
AC
XX
XX 13-FEB-2002 (first entry)
XX
DB Enterococcus faecalis DNA for cellular proliferation protein #338.
XX
XX Antisense; ds; prokaryotic cellular proliferation gene;
KW antibiotic; antibacterial; drug design.
XX
OS Enterococcus faecalis.

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XX WO200170955-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
PF 21-MAR-2001; 2001WO-US09180.
XX
XX 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-207272P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
XX (ELIT-7) ELITRA PHARM INC.
PA
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Traxlick JD, Carr GT;
PI Yamamoto RT, Xu HH;
XX WPI. 2001-611495/70.
DR P-PSDB; AAU35051.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
PT
XX Claim 27; Seq ID No 6547; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antipodes capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence encodes an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1524 BP; 484 A; 302 C; 289 G; 449 T; 0 other;

```

```

Query Match      22.1%; Score 58.2; DB 23; Length 1524;
Best Local Similarity 51.2%; Pred. No. 1.6e-07;
Matches 108; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

```

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QY 53 agggatggaatcgcaataattgagaagccattgcttgatgacttctccata 112
DB 416 aaggcttgcgtcttaattatcgaaagccattgcttcgtatgactgtcgaag 475
QY 113 ggcgcacacatactctcttcacacttcaggaagaacaaatataatgancatc 172
DB 476 aattaatgagaataatcggtgcattcttcgaagaagatatcttcgaattgacatt 535
QY 173 tactaggaagaaatcncaglnaaaatcctncaggtttaagggttcaannmagnttttg 232
DB 536 acttaggcaagaatgacccaatataatcttcgacattcgtttccaaataatttttg 595
QY 233 agccaccttngagmngnaentmnganna 263
DB 596 aatcacaatggaacaatcgltacatgataa 626

```

RESULT 5

ID	AA13065	standard; DNA; 32768 BP.
AC	AA13065;	
DT	19-MAR-1999	(first entry)
DE	Enterococcus faecalis	genome contig SEQ ID NO:128.
XX	Enterococcus faecalis;	contig; detection: Enterococcal infection;
KW	vaccine; attenuation;	computer readable medium; ds.
OS	Enterococcus faecalis.	
PN	W09850555-A2.	
XX	12-NOV-1998.	
PD	04-MAY-1998;	98WO-US08985.
PF	14-NOV-1997;	97US-0066009.
PR	06-MAY-1997;	97US-0044031.
PR	16-MAY-1997;	97US-0046555.
XX	(HUMA-) HUMAN GENOME SCI INC.	
PA	Barash SC, Dillon PJ, Kunsch CA;	
PL	WPI; 1999-045171/04.	
DR		
XX		
PT	New isolated Enterococcus faecalis	polynucleotides and polypeptides
PT	- used to develop products for the	detection of Enterococcus and for
PT	use in vaccines for prevention or	attenuation of Enterococcus
PT	infection.	
XX		
PS	Claim 1; Page 767-783; 2084pp;	English.
XX		
CC	A computer readable medium has been	developed which has recorded on it
CC	982 nucleotide sequences isolated	from the Enterococcus faecalis
CC	AA13065; to AA13065 represent these	nucleotide sequences which are
CC	primary nucleotide sequences, also	known as contigs. The computer-based
CC	system can identify fragments of the	Enterococcus faecalis genome with
CC	commercial importance. The products	can be used to detect the presence
CC	of Enterococcus faecalis in samples.	They can also be used for
CC	diagnosing Enterococcal infection	in an animal and monitoring
CC	progression of disease, and for	identifying agents which can be used
CC	to modulate the growth or	pathogenicity of Enterococcus
CC	another related organism, in vivo	or in vitro. In particular the
CC	polypeptides encoded by the	Enterococcus faecalis nucleotide
CC	sequences can be used in vaccines	to prevent or attenuate an
CC	Enterococcal infection.	
XX		
SO	Sequence 32768 BP; 9529 A; 6883 C;	5611 G; 10720 T; 25 other;
XX		
Query Match	22.1%;	Score 58.2; DB 20; Length 32768;
Best Local Similarity	51.2%;	Pred. No. 4.2e-07;
Matches 108; Conservative	0;	Mismatches 103; Indels 0; Gaps 0;
0Y	53 aggaatggaatcgcataatttggagccatttggcttgcataatccacata	112
Db	19293 aagcttgcatacgtcctaattatcgaaagccattggttcgattatgaatcgtcctacg	19352
0Y	113 ggcgcacacataatcttcttccaacttcgaggaagaacaaatatatgaatgncatc	172
Db	19353 aattaatgaagaatttcgtcgtcattccctcgaaacaagatatcttccgaattggccatt	19412
0Y	173 tactaggaagaatcncgltnaaaatccctncaggtttaagggttcaaanmagtttg	232
Db	19413 acttaggcgaagaatgatcccaaaatatttccagccatcgcttggccataataattttg	19472
0Y	233 agccaccttngagngnagcnnnnnganna	263

D6	19473	aatcacaatggaacaaatcgcttaccattgataa	19503
<hr/>			
RESULT 6			
ID	AAH54037	standard; DNA; 3015 BP.	
XX	AAH54037		
AC	AAH54037;		
XX			
DT	03-SEP-2001 (first entry)		
XX			
DE	S. epidermidis genomic polynucleotide sequence SEQ ID NO:3401.		
XX			
KM	Staphylococcus epidermidis SRI strain; infection; diagnosis;		
XX	vaccination; endocarditis; ds.		
OS	Staphylococcus epidermidis.		
PN	WO200134809-A2.		
XX			
PD	17-MAY-2001.		
PF	09-NOV-2000; 2000WO-US30782.		
XX			
PR	09-NOV-1999; 99US-0164258.		
XX	(GLAX) GLAXO GROUP LTD.		
PA			
XX	Kimmerly WJ;		
P1			
DR	WPI; 2001-316495/33.		
XX			
PT	Nucleic acids encoding polypeptides from Staphylococcus epidermidis,		
PS	useful for vaccinating against infections, e.g. endocarditis -		
XX			
PS	Claim 8; Page 957-958; 2188bp; English.		
CC	AAH52304 to AAH59970 represent nucleic acids (I) encoding polypeptides		
CC	(II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.		
CC	(I) and (II) can have antibacterial activity and therefore can be used		
CC	in vaccination. The nucleic acids (I) may be used to produce the		
CC	S. epidermidis polypeptides (II) via the production of vectors		
CC	containing them which are used to produce hosts cells which express the		
CC	polypeptides. The polypeptides (II) (and/or nucleic acids) may then be		
CC	used to vaccinate subjects and to raise antibodies against the bacteria.		
CC	The polypeptides may also be used to assay for other inhibitors of their		
CC	activity and therefore identify compounds that may be used for the		
CC	treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to		
CC	AAH55090 represent specifically claimed S. epidermidis genomic DNA		
CC	polynucleotide sequences from the present invention. AAH55091 to		
CC	AAH55098 represent oligonucleotide sequences and primers which are used		
CC	in the exemplification of the present invention.		
CC	N.B. the present invention specifically claims all the polynucleotide		
CC	sequences given in the sequence listing of the present specification,		
CC	however the sequence listing only goes up to SEQ ID NO:4454 so even		
CC	though sequences are given in the disclosure for SEQ ID NO:4455 to 4472,		
CC	no sequences are present for SEQ ID NO:4455 to 4464.		
XX			
SO	Sequence 3015 BP; 1138 A; 384 C; 515 G; 978 T; 0 other:		
<hr/>			
Query Match 20.5%; Score 54; DB 22; Length 3015;			
Best Local Similarity 54.5%; Pred. No. 3.5e+06;			
Matches 114; Conservative 0; Mismatches 93; Indels 2; Gaps 1;			
OY	45	gaccagaagygatgaaatcgcatataatgttgagaagccattggctttgatgcatttc	104
DB	1315	gaactgaagaagggygatgcagataatatagaaaacacatttgttgattgatttaaatc	1374
OY	105	ttccatagtgcctgcaacaatatctcttccaacttttagaagaagcaaatatataagat	164
DB	1375	t--gaaaaaatlaatatatacaataaagaagctctttaagaagaanaaaatatttggat	1432

PI Yamamoto RT, Xu HH:
 XX
 DR WPI: 2001-611495/70.
 DR P-PSDB: AA034013.
 XX
 PT New polynucleotides for the identification and development of
 XX antibiotics, comprise sequences of antisense nucleic acids -
 PS
 Claim 27; Seq ID No 4454; 511pp; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
 CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence encodes an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 Sequence 1461 BP; 521 A; 231 C; 257 G; 452 T; 0 other:

```

Query Match Summary      19.5%; Score 51.4; DB 23; Length 1461;
Best Local Similarity    51.0%; Pmed. No. 1.6e-05;
Matches 103; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

OY  52 aaggatggaacgcataatatatttgaagaagccattggcttgatgcacttcctcccat 111
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  415 aaagatttaaacgcttgttatcgaaaaaccattcgtgaagtatttaaatcaagcggaa 474
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY  112 aggcctgaccaatatacctttccaaccttcsgaaaagcaatatagaaattgancat 171
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  475 gcaatnaaacatcaaatctgtaataatcatttaaagaagaagaattatctgatcgaccac 534
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY  172 ctactagaagaagcaatcnasgnanaaacctncaagtttaggttccaannagncttc 231
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  535 tatttaggaaaaagacatggttccaatatatcgaggatcatacgttcttgcgaatcgagatt 594
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY  232 gagcacacttngagnnagant 253
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  595 gaaccattatggaataacaat 616
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 11
AAV74364
ID AAV74364 standard; DNA; 16592 BP.
XX AC
XX AAV74364;
AC
DT
XX
DE
Staphylococcus aureus contig SEQ ID #53.
KW Computer readable medium; Vaccine; S.aureus infection; Immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
XX
OS Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT misc_feature 121..180
```

[illegible]

WPI; 2000-282222/24.

PT Novel methods for screening for antibacterial agents, useful for
PT treatment or prevention of *Staphylococcus* infection, by testing
PT compounds against, essential bacterial genes -
xx

PS Disclosure; Column 35-38; 256pp; English.
vxy

CC The present sequence represents an essential *Staphylococcus aureus* gene
CC The invention relates to a method for screening for an antibacterial
CC agent. The method comprises determining if a test compound is active
CC against the essential bacterial genes (AA26850-A26956). The invention
CC also includes a method for evaluating an agent for activity on the
CC essential genes. Also included in the invention is the production of an
CC antibacterial agent. The antibacterial agents of the invention are used
CC to treat or prevent bacterial infections, particularly where caused by
CC *Staphylococcus aureus*. The antibacterial agents are unlikely to be
CC affected by known resistance mechanisms.

Sequence 2494 BP; 809 A; 396 C; 389 G; 880 T; 20 other;

Query Match	19.28; Score 50.6; DB 21; Length 2494;
Post local classification	10.00; Score 49.9; DB 21; Length 2494;

best local similarity	50.0%;	Pred. No. 3.4e-05;
Matches 101;	Conservative 2;	Mismatches 99;
		Indels 0;
		Gaps 0;

QY	52	aagggaaggaatcgcataaattllggaagcaattgctttgaagcaattcttcccat	111
Db	1425	AAAGGATTTAAAGCCCTTGTTATTCGAAAAACCATTCGGTAGTGAATTTAAAAATCACCCGAA	1366
QY	112	agcgtgcacaaatctctcttccaacttcgcgaagaagcaatatatagaattganat	171
Db	1365	GCATTAAACAATCAAAATTCCTAAATCATTTAAAGAAGAAGAAATTTATTCGTATKACACAC	1306
QY	172	ctactaggaaggaatcncaglnaaatcctncaggttlaaggtttccaannmagnttt	231
Db	1305	TATTTAGGAAAAACATGTTCTCAAAATATTCAGGATTTACGTTTGGCAATCCGATGTTT	1246
QY	232	gagccacctngagngmnaent	253
Db	1245	GAACCAATTATGGAATAAACAAT	1224

RESULT 14

ID	standard; DNA; 2494 BP
AAS08003	

AC AAS08003

DT 23-OCT-2001 (first entry)
yy

Staphylococcus aureus essential pathogenic bacterial DNA #3.

Essential bacterial agent; drug screening; ds

OS Staphylococcus aureus.
XY

PN US6228588-B1
XX

PD 08-MAY-2001
XX

09-MAR-1999; 9905-0266417.

PR	15-SEP-1995;	9505-0003798.
PR	22-DEC-1995;	95115-0009102

PK 13-SEP-1996; 9605-0714918.
XX

PA (MCR-) MICROIDE PHARM INC.
XX

PT BENLON B, LEE VJ, MALOULI
XX

WFL; 2001-342009/36.
XX
XX

PT Screening or producing antibacterial agents active against
PT *Staphylococcus aureus* target genes, comprises contacting a cell or a
PT test compound with a gene product or polypeptide that is encoded by
PT essential bacterial genes -
XX
PS Claim 7; Column 35-37; 251pp; English.

CC The sequence represents a DNA encoding a Staphylococcus aureus essential
CC pathogenic bacterial protein. These polynucleotides are useful for
CC screening for and producing antibacterial agents against pathogenic
CC bacteria. A polypeptide that is encoded by an essential bacterial gene
CC can be contacted with a cell or a test compound and the level of activity
CC against the bacterial protein is monitored. The method is used in drug
CC discovery and drug production, particularly for screening and preparing
CC compounds active against Staphylococcus aureus target genes. These
CC compounds are useful for inhibiting the growth of pathogenic bacteria.

5Q Sequence 2494 BP; 809 A; 396 C; 389 G; 880 T; 20 other;

Query Match	19.28;	Score 50.6;	DB 22;	Length 2494
Best Local Start/End	50.08;	End No. 3	48.05	

Matches 101; Conservative 2; Mismatches 99; Indels 0; Gaps 0;

QY	52	aagggaatcggaatcgcgaataattctggaaagcaattggcttggagccttcttccat	111
Db	1425	AAAGGATTTAAAGCCCTGTTATCGAAAAACCATTCGGTAGTGATTTAAATCAGCCGA	1366
QY	112	aggctgcacacatatcttcttcaaaccttcsgaaagcaatatagaaattgancat	171
Db	1365	GCAATTTAAACATCAAAATTCGTATATCATTTTAAAGAAAGAAATTTATCGATTACAGCC	1306
QY	172	ctactaggaaagaaatcncaglnaaatccctncaagtttaagggttccaannnagnttt	231
Db	1305	TATTTAGGAAGAACATGTTTCMAAATATCGAGATTACGTTTGCAGATGCGATGTTT	1246
QY	232	gagcaccttngnngnancat	253
Db	1245	GAACCATTTATGGAATAACAAT	1224

RESULT 15

ID	AAF91534	standard; DNA; 2494 BP.
----	----------	-------------------------

AC AAF91534,
XX

DT 10-MAY-2001 (first entry)

Staphylococcus aureus essential gene #3.

KW Screening; antibacterial; infection; ds.
XY

05 Staphylococcus aureus.
xy

PN 056187541-B1.
XX

PD 13-FEB-2001.
XX

09-MAR-1999; 9905-0265315.

PR	15-SEP-1995;	9505-0003798.
PR	22-DEC-1995:	9511S-0009102

PR 13-SEP-1990; 9605-0/14918.
XX

PA (MCCR-) MICROCID PHARM INC.
XX

XX
P1 bellon B, Lee VJ, Malouin

XX
XX

WFT, TFM
T07/4T08CT-T00Z

PT treatment or prevention of Staphylococcus infection, by testing

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 3, 2002, 07:40:58 ; Search time 185.98 Seconds
(without alignments)
347.358 Million cell updates/sec

Title: US-09-300-482-4

Perfect score: 263

Sequence: 1 gaagacatttgatgttgc.....agangnactnnnnnganna 263

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA: *
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq: *
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PCUS.COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	50.6	19.2	2494	3	US-08-714-918-3 Sequence 3, Appli
C 2	50.6	19.2	2494	4	US-09-265-315-3 Sequence 3, Appli
C 3	50.6	19.2	2494	4	US-09-265-315-3 Sequence 3, Appli
C 4	50.6	19.2	2494	4	US-09-266-417-3 Sequence 3, Appli
C 5	49.6	18.9	1488	3	US-08-962-859A-1 Sequence 1, Appli
C 6	48	18.3	2764	2	US-08-966-963-4 Sequence 4, Appli
7	37.4	14.2	1461	3	US-08-445-463B-5 Sequence 5, Appli
8	37.4	14.2	1461	5	US-08-445-464C-5 Sequence 5, Appli
9	37.4	14.2	1461	5	PCT-US94-03437-5 Sequence 5, Appli
10	37.2	14.1	1455	5	PCT-US94-03437-7 Sequence 7, Appli
11	37.2	14.1	1457	5	PCT-US94-03437-3 Sequence 3, Appli
12	37.2	14.1	1571	3	US-08-445-463B-3 Sequence 3, Appli
13	37.2	14.1	1571	3	US-08-445-464C-3 Sequence 3, Appli
14	37.2	14.1	1696	1	US-07-737-071A-1 Sequence 1, Appli
15	37.2	14.1	1696	1	US-08-022-096-1 Sequence 1, Appli
16	37.2	14.1	1696	3	US-08-445-463B-7 Sequence 7, Appli
17	37.2	14.1	1696	3	US-08-445-464C-7 Sequence 7, Appli
18	33	12.5	2042	2	US-08-933-821-16 Sequence 16, Appli
19	33	12.5	2042	3	US-08-934-494-5 Sequence 5, Appli
20	33	12.5	2042	3	US-08-960-507-16 Sequence 16, Appli
21	33	12.5	2042	3	US-09-143-068-5 Sequence 5, Appli
22	33	12.5	2042	4	US-09-143-707-5 Sequence 5, Appli
23	33	12.5	2042	4	US-09-202-089-5 Sequence 5, Appli
24	33	12.5	2042	4	US-09-136-828-16 Sequence 16, Appli
25	32	12.2	87350	3	US-08-781-891-79 Sequence 79, Appli
26	29.8	11.3	1458	5	PCT-US94-03437-1 Sequence 10, Appli
27	29.8	11.3	1461	1	US-07-596-867C-10 Sequence 10, Appli

28	29.8	11.3	1506	3	US-08-445-463B-1	Sequence 1, Appli
29	29.8	11.3	1506	3	US-08-445-464C-1	Sequence 1, Appli
30	29.8	11.3	1963	5	PCT-US91-07715A-1	Sequence 1, Appli
31	29.8	11.3	1970	1	US-07-596-867C-1	Sequence 1, Appli
32	29.6	11.3	1484	4	US-09-210-168-2	Sequence 2, Appli
33	29.6	11.3	1517	1	US-08-032-869A-1	Sequence 1, Appli
34	29.6	11.3	1517	1	US-08-032-869A-2	Sequence 2, Appli
35	29.6	11.3	1517	1	US-08-472-673-1	Sequence 1, Appli
36	29.6	11.3	1517	1	US-08-472-673-2	Sequence 1, Appli
37	29.6	11.3	1517	1	US-08-475-782-1	Sequence 1, Appli
38	29.6	11.3	1517	1	US-08-475-782-2	Sequence 1, Appli
39	29.6	11.3	1517	2	US-08-472-678-1	Sequence 2, Appli
40	29.6	11.3	1517	2	US-08-472-678-2	Sequence 2, Appli
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44	29.6	11.3	1518	4	US-09-820-764-1	Sequence 1, Appli
45	29.6	11.3	7904	1	US-08-316-229B-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-714-918-3/c
Sequence 3, Application US/08714918
Patent No. 6037123
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Ving
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmidt, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714.918
FILING DATE: September 13, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 232/005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2494 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
US-08-714-918-3

Query Match
Best Local Similarity 50.0%; Score 50.6; DB 3; Length 2494;
Matches 101; Conservative 2; Mismatches 99; Indels 0; Gaps 0;

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RESULT 2
US-09-265-315-3/C
Sequence 3, Application US/09265315
Patent No. 6187541
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Vling J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2494 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-3

Query Match
Best Local Similarity 50.0%; Score 50.6; DB 4; Length 2494;
Matches 101; Conservative 2; Mismatches 99; Indels 0; Gaps 0;

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RESULT 3
US-09-265-315-3/C
Sequence 3, Application US/09265315
Patent No. 6187541
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Vling J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327

APPLICANT: Jakobovits, Edward B.
 APPLICANT: Silen, Joy L.
 APPLICANT: Levy, Mark J.
 APPLICANT: Goodman, Thomas C.
 APPLICANT: Becker, Martin
 APPLICANT: Ullman, Edwin F.
 APPLICANT: Caldwell, Robert M.
 APPLICANT: Bote, Richard R.
 APPLICANT: Barnett, Christopher C.
 TITLE OF INVENTION: Homogenous Immunoassays Using Mutant
 TITLE OF INVENTION: Glucose-6-Phosphate Dehydrogenases
 NUMBER OF SEQUENCES: 124
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dade Behring Inc.
 STREET: 1717 Deerfield Road
 CITY: Deerfield
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60015
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:

RESULT 15
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; Sequence 1, Application US/08022096
; Patent No. 5308770
; GENERAL INFORMATION:
; APPLICANT: JARSOCH, Michael
; APPLICANT: LANG, Gunter
; TITLE OF INVENTION: CLONING AND OVEREXPRESSION OF
; TITLE OF INVENTION: GLUCOSE-6-PHOSPHATE DEHYDROGENASE FROM LECONOSTOC
; TITLE OF INVENTION: DEXTRANSUCS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIKO, Marmelstein, Murray & Oram
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/022,096

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Search completed: July 3, 2002, 07:41:01
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 3, 2002, 07:54:49 ; Search time 796.36 Seconds
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Title: US-09-300-482-14

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Gapop 10.0 , Gapext 1.0

Searched: 1736436 segs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

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Post-processing: Minimum Match 08
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	243	59.3	483	21	AAC38393	Zea mays DNA fragm
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4	195	47.6	477	21	AAC35766	Zea mays DNA fragm
5	175	42.7	1639	21	AAC46021	Arabidopsis thaliana
6	173.4	42.3	1639	21	AAC39123	Arabidopsis thaliana
7	168	41.0	369	21	AAC38311	Zea mays DNA fragm
8	99.2	24.2	1916	18	AAT86035	Brevibacterium flia
9	97.6	23.8	1476	22	AAH65570	C glutamicum codin

10	97.6	23.8	1537	22	AAE71486	Corynebacterium gl
11	97.6	23.8	1575	22	AAE71485	Corynebacterium gl
12	97.6	23.8	2335	22	AAI65505	Nucleotide sequenc
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14	97.6	23.8	349980	22	AAH68529	C glutamicum codin
15	94.4	23.0	1508	23	ABL06613	Drosophila melanog
16	91.2	22.2	1038602	20	AAZ01425	Complete genome se
17	89.8	21.9	1455	23	AAE53320	Haemophilus influe
18	88	21.5	273254	21	AAC81914	Chlamydia pneumoni
19	85.8	20.9	1458	22	AAH52008	Mycobacterium tube
20	83.8	20.4	2310	24	AAE94752	Human DNA sequence
21	80.2	19.6	92834	21	AAH81473	N. meningitidis pa
22	80.2	19.6	349980	21	AAE21544	Neisseria meningit
23	69.2	16.9	14516	20	AAH06748	E. coli O111 antiag
24	69.2	16.9	14516	21	AAZ56375	Escherichia coli f
25	68.8	16.8	1419	23	AAE53371	Enterococcus faeca
26	68.8	16.8	1422	23	AAE53744	Enterococcus faeca
27	67.2	16.4	29912	23	AAE55907	Protonibacterium
28	66.2	16.1	4487	7	AAH60943	Sequence encoding
29	65.6	16.0	2450	20	AAH20537	Polynucleotide seq
30	62.8	15.3	1407	22	AAH53136	S. epidermidis ope
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33	61.2	14.9	1407	23	AAE56087	Salmonella typhi D
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44	57	13.9	2025	20	AAV42965	Streptococcus pneu
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ALIGNMENTS

RESULT 1	
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AC AAC37505;	
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XX	
DT 17-OCT-2000	(first entry)
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XX	
KW Hybridization assay; genetic mapping; gene expression control;	
KW protein identification; signal transduction pathway;	
KW metabolic pathway; promoter; termination sequence; ss.	
XX	
OS Arabidopsis thaliana.	
XX	
PN EP1033405-A2.	
XX	
PD 06-SEP-2000.	
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PF 25-FEB-2000; 2000EP-0301439.	
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PR 31-AUG-1999; 99US-0151438.
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PR 28-OCT-1999; 990S-0161992.
PR 28-OCT-1999; 990S-0161993.
PR 29-OCT-1999; 990S-0162142.

Query Match 63.5%; Score 260.4; DB 21; Length 1753;
Best Local Similarity 78.2%; Pred. No. 2.6e-58;
Matches 312; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

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DB 146 gctgtgattggtcagaaactcctcaacatgacagagaaggtcccatctgt 205
OY 72 tacacaaggaacactccaaggtgagacggtgacggtgacagaggaaggaac 131
DB 206 tacaacagacactcctccaagttgatgacggtgacagagcaaaaggaagcaat 265
OY 132 ctcccgcttaagcgtctcatgaacccgctccttgttaagtccattcagaagcag 191
DB 266 ctccctcttaagcgtctcatgaacccgagctcttgcataagcattcagaagcagc 325
OY 192 gtcgtatcatctcgtcgaacccgagcgcagctgacacaaacatcgcagacccga 251
DB 326 gttattatcatcgtctgtaagcgtgttctccggtgacacacatcgaacccctct 385
OY 252 gctcaacttgagcagggcagctgcatacgaatgagggagacagagtgacagaaac 311
DB 386 gcttatttgagaaagagtgatgtgtgatgtgtaataagatgataagaaact 445
OY 312 gagagagggagaaagcactgagagagcgagccttctatcttgcatgggtctct 371
DB 446 gagagagagaaagccgctggcgagaaagcgttctcctacttgtaatggagttct 505
OY 372 gagagaaagaggtgcccgcagacgcccgtccttgatg 410
DB 506 ggtgtgtaagaaggtgctcgttaatggccatcatgatg 544

RESULT 2

AAC38393
ID AAC38393 standard; DNA; 483 BP.

XX AAC38393;

DT 17-OCT-2000 (first entry)

DE zea mays DNA fragment SEQ ID NO: 20807.

XX Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway; metabolic;
pathway; promoter; termination sequence; corn; ss.

XX zea mays subsp. mays.

XX EP1033405-A2.
XX 06-SEP-2000.
PD XX
XX 25-FEB-2000; 2000EP-0301439.
XX 25-FEB-1999; 990S-0121825.
XX 05-MAR-1999; 990S-0123180.
XX 09-MAR-1999; 990S-0123548.
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XX 30-JUN-1999; 990S-0141287.

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Query Match	59.38;	Score 243;	DB 21;	Length 483;
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Db 177	cgcgatcatgagggcaaaccttgccctcaacattgagagaagaaggttcccatctcgt 236			
QY 71	gtacaacagagacaacctccaaggtgagacgagacggtbcagcgltgcacaaagcagaaagaaa 130			
Db 237	ctacaacagagacaacctccaaggtgagatgagacggtbcagcgltgcacaaaggtcgaagaaa 296			
QY 131	ccctcccggtcctacggttcctcatgagaccgcgcgtccttttgaaagttccattcagaagccag 190			
Db 297	ccctcccggttcttggtttcttcacgaccgcgcgtcctcttgtagcttcattccagaagccccc 356			
QY 191	ggctggtgacatgctcgtctcaagcgcgcgcgcacattgacacgaaacctgcgaagctcgc 250			
Db 357	tgtctgcatcatgctcgtctcaagcgcgcgcgcgttgagaccgaacctgtccagcgtcgc 416			
QY 251	agctcaacttgagacgagggcgcgactgcatcatcgatvggggggaaacgagttgtaacgaataac 310			
Db 417	ggcgacaccttgatcagggggagactgcatcgtcgtatgtgccaacgaggtgtaacgagaacac 476			
QY 311	ggagagag 317			
Db 477	ggagagag 483			

ID AAC1032 standard; DNA; 466 BP.
XX AAC1032;
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DT 17-OCT-2000 (first entry)
XX
DE Zea mays DNA fragment SEQ ID NO: 30405.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic;
KW pathway; promoter; termination sequence; corn; ss.
XX
OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
PD
XX 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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Query Match 59.1%; Score 242.4; DB 21; Length 466;
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DB 212 ggggtatgtgggagaaaccttgcctcaaatgtcagagaaggggtcccatctctgtg 271
OY 72 tacaagagacaacctcctaaggttgagcagacggtgcagcccaaggcagaaggaac 131
DB 272 tacaagagacaacctcctaaggttgagcagacggtgcagcccaaggcagaaggaac 331
OY 132 ctctccgcttaagcgtctcattgaccccgctctcttgaagtcaattcagaagccag 191
DB 332 ctctccgcttaagcgtctcattgaccccgctctcttgaagtcaattcagaagccag 391
OY 192 gtgggagatcatgtctcgtcaagcgcgccgacagttgaccacaacatcgcgagctcga 251
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DB 392 gtgggtatcatgtctcgtcaagcgcgccgacagttgaccaga-catcgcgacgtcga 450
OY 252 gctcaacttgagcagc 267
DB 451 gctcaacttgagcagc 466

RESULT 4
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ID AAC35766 standard; DNA: 477 BP.
AC AAC35766;
XX
DT 17-OCT-2000 (first entry)
DE Zea mays DNA fragment SEQ ID NO: 11344.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic;
KW pathway; promoter; termination sequence; corn; ss.
XX
OS Zea mays subsp. mays.
XX
PN BP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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PR 05-MAR-1999; 99US-0123180.
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Query Match 47.6%; Score 195; DB 21; Length 477;
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 Db 233 cgcggtcatgggagcaaccttgcctcaacatctgcgagagaagggttcccatctcgt 292
 QY 71 gtacaacaggaacaacctccaagtgtagcagaccgtgcagcgtgccaaggcagaaggaaa 130

Db 293 ctacacacagagacacctcaaggtgacagacgctgacgctgcacaggtccgaagga 352
QY 131 cctccgcctcaagcctccatgaccccgctcctcttctgtaagttccatccagaagccag 190
Db 353 cctcccgctgttggttccacgaccccgctcctctgtagctccatccagaagcccg 412
QY 191 ggtggtgatactgctcgtcaagcgcgccgacgttgaccagacatcgacgctcgc 250
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QY 251 agctc 255
Db 473 ggcgc 477

RESULT 5
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ID AAC46021 standard; DNA: 1639 BP.
XX AAC46021:
AC AAC46021:
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 48624.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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QY	71 gtacaacagacgaacctccaaggttggaacgacgltgcacggtgcgaagcgagaagaa	130		
Db	161 ctacaatcgaaacaccttccaagaagtcgacgaacaccttaagctcgtccccaagaagaa	220		
QY	131 ccttcctcgctacagccttcacgaaccccgctcctttgtgaagctcatccagaacgacg	190		
Db	221 acctcccaagctcgtgttcaactactcgcctccgcgatttcgttctctcgatccaagcctcag	280		
QY	191 ggttggtgatcatgctcgtctaaagcgcgcgcgcagttgacacgaacctcgcgcgtcgc	250		
Db	281 atccgcttatcatctctgttcaaacccggtctccctcgttgacaacacctctcgtctctc	340		
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QY	311 ggaagaggaaggaagacatggaagcgcgcgcctcctnctatctcttgcatggtgtctc	370		
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XX		
DT	17-OCT-2000	(first entry)
XX		
DE	Arabidopsis thaliana	DNA fragment SEQ ID NO: 23456.
XX		
KM	Hybridisation assay; genetic mapping; gene expression control;	
KM	protein identification; signal transduction pathway;	
KW	metabolic pathway; promoter; termination sequence; ss.	
XX		
OS	Arabidopsis thaliana.	
XX		
PN	EP1033405-A2.	
XX		
PD	06-SEP-2000.	
XX		
PF	25-FEB-2000; 2000EP-0301439.	
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RESULT 7
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DT 17-OCT-2000 (first entry)
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DE Zea mays DNA fragment SEQ ID NO: 20523.
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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic;
KW pathway; promoter; termination sequence; corn; ss.
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Qy 72 taccaacagacaaacctccaaggttgacagagacgtgcagcgtgccaagcgcaagaaac 131
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ID AAT88035 standard; DNA; 1916 BP.
XX AC
XX AAT88035;
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XX 22-DEC-1997 (first entry)
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XX Brevibacterium flavum 6-phosphogluconate dehydrogenase DNA.
DE
XX Brevibacterium flavum; 6-phosphogluconate dehydrogenase;
KW recombinant production; coryneform; bacterium; bacteria; ds.
XX
XX Brevibacterium flavum.
OS
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XX Key Location/Qualifiers
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XX JF09224662-A.
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PD 02-SEP-1997.
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PF 23-FEB-1996; 96JP-0036346.
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PR 23-FEB-1996; 96JP-0036346.
XX
PA (MITU) MITSUBISHI CHEM CORP.
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XX WPI; 1997-484097/45.
DR P-PSDB; AAM27613.
XX
PT 6-phospho:gluconate dehydrogenase - can be recombinantly produced by
PT transforming coryneform bacteria with DNA molecule encoding it
XX
PS Claim 1; Pages 5-7; 8pp; Japanese.
XX
CC The present sequence encodes the Brevibacterium flavum JM-233
CC 6-phosphogluconate dehydrogenase (6-PD). The 6-PD can be
CC recombinantly produced by transforming coryneform bacteria with the
CC DNA molecule encoding it.
XX
SQ Sequence 1916 BP; 425 A; 596 C; 507 G; 388 T; 0 other;

Query Match 24.2%; Score 99.2; DB 18; Length 1916;
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DB 503 tacaacgcagcactgacaacaaaccgacgcatcgcgcgatcagcgtccggaagcaac 562
OY 132 ctcccgctcgaagcgttcacatgaaccccgctccttgtagaagtcacatcagaacgag 191
DB 563 ttcacaccttcgcgaacccgctcggaag-----tctgtagcaccctctggaagcagc 616
OY 192 gtggtatcatgctcgtcgaagcgcgccaggttgacaagacacatcgagcgtcgca 251
DB 617 cgcgcatacatcattgttcaagctgtgtaacgacacgacgacatcacaacgacgtgca 676
OY 252 gctcacttggagcagagcgactgcatcgcgtgagggggaacgagtgtaacgagaacag 311
DB 677 gacgcattgagcagaagcgacatcatcgcgcgcgcgcgcgcgcctctacacgcgacac 736
OY 312 gaagaagaggaagagcgcacatgagagcgcgccctctgtatcttgcgtggtctct 371
DB 737 attcgctcgagaaagaaatctccgacgcggtctccacttcgctgctgtgtatctct 796
OY 372 ggaggaagagaggtgcccgaacgcccgtcttgatg 410
DB 797 ggcgcgcaagaagcgacatcaacggccatcattcatg 835

RESULT 9
AAH6570
ID AAH6570 standard; DNA; 1476 BP.
XX
AC AAH6570;
XX
DT 26-SEP-2001 (first entry)
XX
DE C glutamicum coding sequence fragment SEQ ID NO: 1605.
XX
KM Corynebacterium; amino acid synthesis; vitamin; saccharide;
XX organic acid synthesis; ds.
XX Corynebacterium glutamicum.
OS
XX
PN EPI108790-A2.

XX
PD 20-JUN-2001.
XX
PF 18-DEC-2000; 2000BP-0127688.
XX
PR 16-DEC-1999; 99JP-0377484.
XX
PR 07-APR-2000; 2000JP-0159162.
XX
PR 03-AUG-2000; 2000JP-0280988.
XX
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX
XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
DR WPI; 2001-376931/40.
XX
DR P-PSDB; AAC91351.
XX
PT Novel polynucleotides derived from Corynebacterium bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analysing
PT expression profile or pattern of a gene and identifying homologous gene
XX
PS Claim 8; SEQ ID NO: 1605; 246pp + Sequence Listing; English.

XX
CC The present invention provides a number of nucleotide and protein
CC sequences from the Corynebacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of coryneform bacterium, measuring expression amount and
CC analysing the expression profile or expression pattern of a gene derived
CC from Corynebacterium, and identifying a homologue of a gene derived
CC from Corynebacterium. Corynebacterium bacteria are useful for producing
CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC European Patent Office.
XX
SQ Sequence 1476 BP; 328 A; 489 C; 382 G; 277 T; 0 other;

Query Match 23.8%; Score 97.6; DB 22; Length 1476;
Best Local Similarity 54.6%; Pred. No. 5.9e-16;
Matches 218; Conservative 0; Mismatches 175; Indels 6; Gaps 1;

OY 12 ggcgtatcgtggcagaaacttcgacctcaacattgcagagagaaggtcccatctgtg 71
DB 70 gaagtaatggtctcaaacctcgccgcaacttcgcccgaacgacacacatcgtcgtgtc 129
OY 72 tacaagaagcaaacctcgaaggtgagagacggtgcagcgtgccaagcagaagaagaaac 131
DB 130 tacaacgcagcactgacaacaaaccgacgcatcgcgcgcgcgcgcgcctctacacgcgac 189
OY 132 ctcccgctcgaagcgttcacatgaaccccgctccttgtagaagtcacatcagaacgag 191
DB 190 ttcacaccttcgcgaacccgctcggaag-----gtctgtagcaccctctggaagcagc 243
OY 192 gtggtatcatgctcgtcgaagcgcgccaggttgacaagacacatcgagcgtcgca 251
DB 244 cgcgcatacatcattgttcaagctgtgtaacgacacgacgacatcacaacgacgtgca 303
OY 252 gctcacttggagcagagcgactgcatcgcgtgagggggaacgagtgtaacgagaacag 311
DB 304 gatgcattgagcagaagcgacatcatcgcgcgcgcgcgcgcgcctctacacgcgacac 363
OY 312 gaagaagaggaagagcgcacatgagagcgcgccctctgtatcttgcgtggtctct 371
DB 364 attcgctcgagaaagaaatctccgacgcggtctccacttcgctgctgtgtatcttc 423
OY 372 ggaggaagagaggtgcccgaacgcccgtcttgatg 410
DB 424 ggcgcgcaagaagcgacatcaacggccatcattcatg 462

```
RESULT 10
AA71486
ID AAF71486 standard; DNA; 1537 BP.
XX
AC AAF71486;
XX
DT 30-APR-2001 (first entry)
XX
DE Corynebacterium glutamicum SMP protein nucleotide sequence SEQ ID NO:253.
XX
KW Corynebacterium glutamicum: carbon metabolism and energy production;
KW SMP protein; sugar metabolism and oxidative phosphorylation protein;
KW fine chemical production; organic acid; proteinogenic amino acid;
KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;
KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;
KW carbohydrate; aromatic compound; vitamin; cofactor; polypeptide; enzyme;
KW diagnosis; Corynebacterium diphtheriae; evolutionary study; ds.
XX
OS Corynebacterium glutamicum.
XX
MN W020100844-A2.
XX
PD 04-JAN-2001.
XX
PE 23-JUN-2000; 2000KO-IB00943.
XX
PR 25-JUN-1999; 9905-0141031.
PR 08-JUL-1999; 99DE-1031412.
PR 08-JUL-1999; 99DE-1031413.
PR 08-JUL-1999; 99DE-1031419.
PR 08-JUL-1999; 99DE-1031420.
PR 08-JUL-1999; 99DE-1031428.
PR 08-JUL-1999; 99DE-1031431.
PR 08-JUL-1999; 99DE-1031433.
PR 08-JUL-1999; 99DE-1031434.
PR 08-JUL-1999; 99DE-1031510.
PR 08-JUL-1999; 99DE-1031562.
PR 08-JUL-1999; 99DE-1031634.
PR 09-JUL-1999; 99DE-1032180.
PR 09-JUL-1999; 99DE-1032227.
PR 09-JUL-1999; 99DE-1032230.
PR 09-JUL-1999; 9905-0143208.
PR 14-JUL-1999; 99DE-1032924.
PR 14-JUL-1999; 99DE-1032973.
PR 14-JUL-1999; 99DE-1032975.
PR 27-AUG-1999; 99DE-1033003.
PR 31-AUG-1999; 99DE-1040765.
PR 03-SEP-1999; 99DE-1042076.
PR 03-SEP-1999; 99DE-1042079.
PR 03-SEP-1999; 99DE-1042086.
PR 03-SEP-1999; 99DE-1042087.
PR 03-SEP-1999; 99DE-1042088.
PR 03-SEP-1999; 99DE-1042095.
PR 03-SEP-1999; 99DE-1042123.
PR 03-SEP-1999; 99DE-1042125.
XX
PA (BAD1 ) BASF AG.
XX
PI Pompejus M, Kroegeer B, Schroeder H, Zelder O, Haberhauer G;
XX
DR P-PSDB; AAB79369.
XX
PT WPI; 2001-061975/07.
XX
PT New isolated Corynebacterium glutamicum nucleic acid encoding a sugar
XX metabolism and oxidative phosphorylation protein for production or
XX modulation of production of fine chemicals e.g. amino acids,
XX carbohydrates or enzymes -
XX
PS Claim 3; Page 504-506; 1246pp; English.
XX
CC AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
```

```
CC metabolism and oxidative phosphorylation (SMP) proteins given in
CC AAF79243 to AAB 79633 which are involved in carbon metabolism and
CC energy production. The C. glutamicum SMP gene can be used in vectors
CC (II) for expression in host cells and production or modulation of
CC production of fine chemicals, such as, an organic acid, a proteinogenic
CC or nonproteinogenic amino acid (preferred), a purine or pyrimidine base,
CC a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty
CC acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a
CC cofactor, a polypeptide, or an enzyme. The presence of (I) or SMP proteins
CC (III) encoded by them are used for diagnosing the presence or activity of
CC Corynebacterium diphtheriae in a subject. (I), (II), (III) or host cells
CC containing them are used to map genomes of organisms related to
CC C. glutamicum, identify and localize C. glutamicum sequences of interest,
CC in evolutionary studies, in determining SMP protein regions required
CC for function, in modulating SMP protein activity, in modulating the
CC metabolism of sugars, and in modulating high-energy molecule production
CC in a cell (i.e. ATP, NADPH).
XX
SQ Sequence 1537 BP; 341 A; 512 C; 392 G; 292 T; 0 other:
XX
Query Match 23.8%; Score 97.6; DB 22; Length 1537;
Best Local Similarity 54.6%; Pred. No. 6e-16;
Matches 218; Conservative 0; Mismatches 175; Indels 6; Gaps 1;
QY 12 gcgcgtacggagcaaaccttgcctcaacatgtcagagagaaggttcccatctgtg 71
Db 146 gcagtaatgtgtcacaacccctgcgcgaacttgcgcgaacgcaacatgtcgtctc 205
QY 72 tacacaggaacaacctcaaggttgacgagacggtgcagcgttccaaggaagaagaac 131
Db 206 tacacacgcgcacatgacaacaacgaagctcatcgccgaltcacggtcccgaaagc 265
QY 132 ctcccgctcagcgttcacatgaccccgctccttctgtgaagtcattcagaagcagcg 191
Db 266 ttaatccctctcgaacgctcgaaga-----gtcgttgcaacctctggaagcaccg 319
QY 192 gtgtgcatcgtctcgtcaagcgcgcgcgttgacagacacatcgcgcagcgtcga 251
Db 320 cgcgcacatcgtcgttgcaggtgttaacgcacagcagcagtcataccacgcgtgca 379
QY 252 gtcactttggaagagcgactcatcatcgatggggggaacgagttgtaagaagaacg 311
Db 380 gatgcacatggaagagcgacatcatcatcagcagcggaacccctcaccacgcgacc 439
QY 312 gaagaggaaggaagggccatgagagcgcgccctctgtacttggcatgggtgtctc 371
Db 440 attcgtcgcgagaagaatctccgacgcggtctccactcgtcgtgtgtatctcc 499
QY 372 ggaagaaagaggtgtccgcgaacgcccgtcttgatg 410
Db 500 ggcgcggaagaagcgcatcacaagcccatcatatg 538
RESULT 11
AA71485
ID AAF71485 standard; DNA; 1575 BP.
XX
AC AAF71485;
XX
DT 30-APR-2001 (first entry)
XX
DE Corynebacterium glutamicum SMP protein nucleotide sequence SEQ ID NO:251.
XX
KW Corynebacterium glutamicum: carbon metabolism and energy production;
KW SMP protein; sugar metabolism and oxidative phosphorylation protein;
KW fine chemical production; organic acid; proteinogenic amino acid;
KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;
KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;
KW carbohydrate; aromatic compound; vitamin; cofactor; polypeptide; enzyme;
KW diagnosis; Corynebacterium diphtheriae; evolutionary study; ds.
XX
OS Corynebacterium glutamicum.
```


PN	MOZ00100844-A2.
XX	
XX	04-JAN-2001.
XX	
XX	23-JUN-2000; 2000MO-IB00943.
XX	
PR	25-JUN-1999; 99US-0141031.
PR	08-JUL-1999; 99DE-1031412.
PR	08-JUL-1999; 99DE-1031413.
PR	08-JUL-1999; 99DE-1031419.
PR	08-JUL-1999; 99DE-1031420.
PR	08-JUL-1999; 99DE-1031424.
PR	08-JUL-1999; 99DE-1031428.
PR	08-JUL-1999; 99DE-1031431.
PR	08-JUL-1999; 99DE-1031433.
PR	08-JUL-1999; 99DE-1031434.
PR	08-JUL-1999; 99DE-1031510.
PR	08-JUL-1999; 99DE-1031562.
PR	08-JUL-1999; 99DE-1031634.
PR	09-JUL-1999; 99DE-1032180.
PR	09-JUL-1999; 99DE-1032227.
PR	09-JUL-1999; 99DE-1032230.
PR	09-JUL-1999; 99US-0143208.
PR	14-JUL-1999; 99DE-1032924.
PR	14-JUL-1999; 99DE-1032973.
PR	14-JUL-1999; 99DE-1033005.
PR	27-AUG-1999; 99DE-1040765.
PR	31-AUG-1999; 99US-0151572.
PR	03-SEP-1999; 99DE-1042076.
PR	03-SEP-1999; 99DE-1042079.
PR	03-SEP-1999; 99DE-1042086.
PR	03-SEP-1999; 99DE-1042087.
PR	03-SEP-1999; 99DE-1042088.
PR	03-SEP-1999; 99DE-1042095.
PR	03-SEP-1999; 99DE-1042123.
XX	03-SEP-1999; 99DE-1042125.
XX	
PA	(BADI) BASF AG.
XX	
PI	Pompejus M, Kroegeer B, Schroeder H, Zeldner O, Habernauer G;
XX	
DR	WPI; 2001-061975/07.
DR	P-PSDB; AAB79368.
PT	
PT	New isolated Corynebacterium glutamicum nucleic acid encoding a sugar
PT	metabolism and oxidative phosphorylation protein for production or
PT	modulation of production of fine chemicals e.g. amino acids,
XX	carbohydrates or enzymes -
XX	
PS	Claim 3; Page 500-502; 1246pp; English.
XX	
CC	AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
CC	metabolism and oxidative phosphorylation (SMP) proteins given in
CC	AAB79243 to AAB 79633 which are involved in carbon metabolism and
CC	energy production. The C. glutamicum SMP gene can be used in vectors
CC	(II) for expression in host cells and production or modulation of
CC	production of fine chemicals, such as, an organic acid, a protinogenic
CC	or nonprotinogenic amino acid (preferred), a purine or pyrimidine base,
CC	a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty
CC	acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a
CC	cofactor, a polypeptide, or an enzyme. The presence of (I) or SMP proteins
CC	(III) encoded by them are used for diagnosing the presence or activity of
CC	Corynebacterium diptheriae in a subject. (I), (II), (III) or host cells
CC	containing them are used to map genomes of organisms related to
CC	C. glutamicum, identify and localise C. glutamicum sequences of interest,
CC	in evolutionary studies, in determinning SMP protein regions required
CC	for function, in modulating SMP protein activity, in modulating the
CC	metabolism of sugars, and in modulating high-energy molecule production
CC	in a cell (I.e. ATP, NADPH).
XX	
SO	Sequence 1575 BP; 352 A; 521 C; 399 G; 303 T; 0 other.

	Query Match	23.8%	Score 97.6:	DB 22:	Length 1575:				
	Best Local Similarity	54.6%	Pred. No. 6e-16:						
	Matches 218:	Conservative	0:	Mismatches 175:	Indels 6:				
					Gaps 1:				
QY	12	gcgctcatgggacgaaccttgcctccaacattgcagagaagggcttcccatctctgtg	71						
DB	146	gaagtaatgggtctcaaaccttgcgcgaaccttgcgccgaagcgcaaacactgtctgtc	205						
QY	72	tacacagacacacctccaaggtgacgagaccgtgcagctgtgccaaagcagaaggaac	131						
DB	206	tacacacgcgacgacacgcacaaacgcagaagctcatatgcgcgaltcacggtctcgaaggaac	265						
QY	132	cttccgcgtctacggtcttcattgaccccgctctcttgtgaagttcatctcaagaagccag	191						
DB	266	ttcatctcctcttgcacaaccgtcgaga-----gttcgtatgacctcttgaagaagccagc	319						
QY	192	gtgctgcatcatgtctgtccaagcgccgcgcgcagcttgaccacaacatcgcgcgtctgca	251						
DB	320	cgcgcacatcatcatgtgtctgacgtctgttaagccaccgacgcagctcatcaaccagctgca	379						
QY	252	gctcaacttggacagggcgactgcatactcgatgggggaacgagtgtgacgagaacag	311						
DB	380	gatgccatggacgaaggcgacatcatctacgcgcgcgcgcgcgcctcaccgcgacacc	439						
QY	312	gagagagaggaagagccctcgtgagagcgccgctctctgtatcttggcattggtgtctct	371						
DB	440	atctgtctcgagaaagaaatctccgcagcggtctcccaacttctgtggtctgtatctcc	499						
QY	372	gagagaaagagaggtgctccgcgaacgcgcgtctctgtatg	410						
DB	500	gcgcgcgaagaaagcgcaactcaacgcgcacatcatcatg	538						
RESULT 12									
AA165505	AA165505 standard; DNA; 2335 BP.								
XX	AA165505;								
AC									
XX	10-DEC-2001 (first entry)								
DE	Nucleotide sequence of the Corynebacterium gnd gene.								
XX									
KW	gnd gene; 6-phosphogluconate dehydrogenase; L-amino acid; L-lysine;								
KW	L-threonine; L-tyrocinophan; ss.								
OS	Corynebacterium glutamicum.								
XX									
XX	Key	Location/Qualifiers							
FT	CDS	474..1853							
FT		/*tag= a							
FT		/product= "6-phosphogluconate dehydrogenase"							
XX									
PN	WO200171012-A1.								
XX									
PD	27-SEP-2001.								
XX									
PE	05-JUL-2000; 2000WO-EP06299.								
XX									
PR	20-MAR-2000; 2000US-0531265.								
XX									
PA	(DEGS) DEGUSSA AG.								
XX									
PA	(UYNA-) UNITV NAT IRELAND.								
XX									
PI	Dunicao UK, McCormack A, Stapelton C, Burke K, Moeckel B.								
XX									
DR	WPI; 2001-602792/68.								
XX									
DR	P-PSDB; AAG73095.								
XX									
PT	Preparing L-amino acids by fermenting coryneform bacteria transformed								
PT	with the 6-phosphogluconate dehydrogenase gene is particularly useful								
PT	to produce L-lysine and L-threonine								

```

XX XX Example 2; Page 43-46; 59pp; English.
PS CC The present sequence represents the gnd gene of Corynebacterium
XX CC glutamicum. The gnd gene encodes a 6-phosphogluconate dehydrogenase
CC enzyme. The gnd gene is used to produce recombinant bacteria for use
CC in the course of the invention. The specification describes a method
CC for the fermentative preparation of L-amino acids, in particular
CC L-lysine, L-threonine, and L-tryptophan. The method comprises fermenting
CC coryneform bacteria in which the gnd gene is amplified and overexpressed.
CC The L-amino acids produced are used in animal nutrition, human medicine
CC and the pharmaceuticals industry.
SQ Sequence 2335 BP; 533 A; 695 C; 606 G; 501 T; 0 other;

Query Match          23.8%; Score 97.6; DB 22; Length 2335;
Best Local Similarity 54.6%; Pred. No. 6.7e-16;
Matches 218; Conservative 0; Mismatches 175; Indels 6; Gaps 1;

QY 12 ggcgtcatgaggcagaacctgcctcaacaltgcagagaagggtcccatctgtg 71
DB 11 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 543 gcaatgatggtcacaacctgcctcaacaltgcctgcagcgaagcaacatgtgtc 602
QY 72 taacaagagaacaacctccaaggtgagcagcagcgtgccaaggcagaagaac 131
DB 11 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 603 taacaacgcagacacgacaacaaacgcagacatcgcgcgaacagcgtccgaagc 662
QY 133 ctcccgcttaagcgttcacatgaccccgctcctgttgaggtccatcagaagcag 191
DB 11 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 663 ttcatccctctgcacacgcgtcgaga-----gttcgttagcattccctggaagcagc 716
QY 192 gtggtgcatcagctcgtcaaggcgcgcgcgcaggttgacacacatcgacacgcga 251
DB 11 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 717 cgcgcacacacacatcagttcagcgtgtgtaacgcaccgcagcagcatcaacacagctgca 776
QY 252 gctcaacttgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 311
DB 11 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 777 gatgcacatgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 836
QY 312 gagaggaaggagagcagcagcagcagcagcagcagcagcagcagcagcagc 371
DB 11 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 837 attcgtcgcagaggaagaaatctccgcacgcgtctccacttcgtcgtgctatctcc 896
QY 372 ggaaggaaggaggtgcccgcagcagcagcagcagcagcagcagcagcagcag 410
DB 11 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 897 ggcgcgcagaggaagcagcagcagcagcagcagcagcagcagcagcagcagc 935

RESULT 13
AAH68528/c
ID AAH68528 standard; DNA; 349980 BP.
XX
XX AAH68528;
AC
XX 26-SEP-2001 (first entry)
DE C glutamicum coding sequence fragment SEQ ID NO: 7063.
XX
XX DE
XX KM Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
XX organic acid synthesis; ds.
XX OS Corynebacterium glutamicum.
XX PN EP1108790-A2.
XX
XX PD 20-JUN-2001.
XX
XX PF 18-DEC-2000; 2000EP-0127688.
XX
XX PR 16-DEC-1999; 99JP-0377484.
XX 07-APR-2000; 2000JP-0159162.
XX PR 03-AUG-2000; 2000JP-0280988.

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XX XX (KYOW ) KYOWA HAKKO KOGYO KK.
PA
XX PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
XX PI Tetsuishi N, Senoh A, Ikeda M, Ozaki A;
XX DR WPI: 2001-376931/40.
XX
XX PT Novel polynucleotides derived from Coryneform bacteria, for identifying
XX PT mutation point of a gene, measuring expression of a gene, analysing
XX PT expression profile or pattern of a gene and identifying homologous gene
XX PT
PS Disclosure; SEQ ID NO: 7063; 246pp + Sequence Listing; English.
XX
XX CC The present invention provides a number of nucleotide and protein
XX CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
XX CC are useful for identifying the mutation point of a gene derived from a
XX CC mutant of coryneform bacterium, measuring expression amount and
XX CC analysing the expression profile or expression pattern of a gene derived
XX CC from Coryneform bacterium, and identifying a homologue of a gene derived
XX CC from coryneform bacterium. Coryneform bacteria are useful for producing
XX CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
XX CC particularly L-lysine. The present sequence is a nucleic acid described
XX CC in the exemplification of the invention.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from the
XX CC European Patent Office.
SQ Sequence 349980 BP; 80727 A; 91049 C; 97618 G; 80586 T; 0 other;

Query Match          23.8%; Score 97.6; DB 22; Length 349980;
Best Local Similarity 54.6%; Pred. No. 2.4e-15;
Matches 218; Conservative 0; Mismatches 175; Indels 6; Gaps 1;

QY 12 ggcgtcatgaggcagaacctgcctcaacaltgcagagaagggtcccatctgtg 71
DB 11 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 331747 GCAGTAAATGGGCTCAAAACCTCCGCCCAACTTCGCCGGAAGGCAACAGTGCCTGTC 331688
QY 72 taacaagagaacaacctccaaggtgagcagcagcagcagcagcagcagcagcagc 131
DB 11 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 331687 TACAAACGCAAGCACTGACAAAACGCAAGCTATCGCGATCACGGCTCCGAAGCAAC 331628
QY 133 ctcccgcttaagcgttcacatgaccccgctcctgttgaggtccatcagaagcag 191
DB 11 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 331627 TTCATCCCTTCGCAACCGTCAAGA-----GTTCTGTAAGCATCCCTGGAAGAGCCACGC 331574
QY 192 gtggtgcatcagctcgtcaaggcgcgcgcgcaggttgacacacatcgacacgcga 251
DB 11 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 331573 CCGCGCATCATCATGTTTCAGGCTGTAAAGCCACGACGCAAGTCATCAACCACTGGCA 331514
QY 252 gctcaacttgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 311
DB 11 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 331513 GATGCCATGCAAGAGGAGACATCATCAAGCGGCAAGCGCCCTTACACACCAACAC 331454
QY 312 gagaggaaggagagcagcagcagcagcagcagcagcagcagcagcagcagc 371
DB 11 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 331453 ATTGCTCGGAGAGAAATGTCGCAAGCGGTCTCCACTTCGTGCTGCTGTAATCTCC 331394
QY 372 ggaaggaaggaggtgcccgcagcagcagcagcagcagcagcagcagcagcag 410
DB 11 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 331393 GCGCGCAAGAAAGCGCACTCAACGGCCCATCATCATG 331355

RESULT 14
AAH68529/c
ID AAH68529 standard; DNA; 349980 BP.
XX
XX AAH68529;
AC
XX 26-SEP-2001 (first entry)
DE
XX
XX DE
XX KM
XX organic acid synthesis; ds.
XX OS
XX PN
XX EP1108790-A2.
XX
XX PD
XX
XX PF
XX
XX PR
XX
XX PR

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DE C glutamicum coding sequence fragment SEQ ID NO: 7064.
XX
KM Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
KM organic acid synthesis; ds.
OS
XX Corynebacterium glutamicum.
PN
XX EPI108790-A2.
PD
XX 20-JUN-2001.
PF
XX 18-DEC-2000; 2000EP-0127688.
XX
XX 16-DEC-1999; 99JP-0377484.
PR 07-APR-2000; 2000JP-0159162.
PR 03-AUG-2000; 2000JP-0280988.
XX
XX (KYOW) KYOWA HAKKO KOGYO KK.
PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX
XX WPI; 2001-376931/40.
XX
XX Novel polynucleotides derived from Coryneform bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analysing
PT expression profile or pattern of a gene and identifying homologous gene
XX
XX
PS Disclosure: SEQ ID NO: 7064; 246bp + Sequence Listing; English.
XX
XX The present invention provides a number of nucleotide and protein
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of coryneform bacterium, measuring expression amount and
CC analysing the expression profile or expression pattern of a gene derived
CC from Coryneform bacterium, and identifying a homologue of a gene derived
CC from coryneform bacterium. Coryneform bacteria are useful for producing
CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC European Patent Office.
XX
XX Sequence 349980 BP; 82466 A; 95954 C; 90516 G; 81044 T; 0 other;
SQ
Query Match 23.8%; Score 97.6; DB 22; Length 349980;
Best Local Similarity 54.6%; Pred. No. 2,4e-15;
Matches 218; Conservative 0; Mismatches 175; Indels 6; Gaps 1;
QY 12 ggggtcattggggcagaacctgtccctcaacattgcagagaagggtcccatctctgtg 71
DB 31747 GCGATTATGAGGCTCAAACTCGCCGCACTTGCCTCCGCAACGGCAACACTGCTGCTC 31688
QY 72 tacaacaggaacaacctcgaaggtgacagacgltgacagcgtgccaagcagaaggaac 131
DB 31687 TACACCGCAGCACTGCAAAACCGACACACTCCTCCGATCAGGCTCCGAAGGCAAC 31628
QY 132 ctcccgctcagcgtctccatgaccccgctccttctgtgaagtcattcagaagccagc 191
DB 31627 TTTCATCCCTTCTGCACACCGTCGAAGA-----GTTCTAGCATCCTCGAAMAAGCCACGC 31574
QY 192 gtggtgatcatgtctgccaagcgccgagcgccagltgaccaagaccatcgagactcgca 251
DB 31573 CCGCGCATCTCATGCTTCAGGCTGTTACGCCACCGACGACGATCATCAACCACTGCA 31514
QY 252 ggcacttggagagcgagctgcatcatcgatcgatgaggaagcgtgtgtcagaagaagc 311
DB 31513 GATGCCATGACGAAGCGCAGCATCATCATGACGCGGCAACGCCCTCTACACCGCAACC 31454
QY 312 gagagagaggaagagccatgagagcgcgcctnctgtatcttggcatgagtgctct 371

DB 31453 ATTGCTCGCAGAGAAATCTCCGACAGCGGTCTCCACTCTGCTGATCTCC 31394
QY 372 ggaggaagagaggtgtcccgcaagcgccgtcctgtgtg 410
DB 31393 GCGCGGAGAGAGGCGCATCTCAACGCCCATCATCATG 31355
RESULT 15
ABL06613
ID ABL06613 standard; cDNA; 1508 BP.
XX
XX ABL06613;
AC
XX 26-MAR-2002 (first entry)
DT
XX
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 14321.
DE
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
XX Drosophila melanogaster.
OS
XX
XX WO200171042-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
XX 23-MAR-2001; 2001WO-US09231.
PF
XX
XX 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
PR
XX
XX (PEKE) PE CORP NY.
PA
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
PI WPI; 2001-656860/75.
DR
XX
XX P-PSDB; ABB62510.
DR
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
PT
XX
XX
XX Claim 1; SEQ ID NO 14321; 21pp + Sequence Listing; English.
PS
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB5737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at http://wipo.int/pub/published_pcl_sequences.
XX
XX Sequence 1508 BP; 328 A; 443 C; 464 G; 273 T; 0 other;
SQ
Query Match 23.0%; Score 94.4; DB 23; Length 1508;
Best Local Similarity 54.1%; Pred. No. 4.1e-15;
Matches 216; Conservative 0; Mismatches 177; Indels 6; Gaps 1;
QY 12 ggggtcattggggcagaacctgtccctcaacattgcagagaagggtcccatctctgtg 71
DB 99 ggcgtcatgtggcacaacctgatctcaatgacgagagagattcgtgtgtgtgtgccc 158
QY 72 tacaacaggaacaacctcgaaggtgacagacgltgacagcgtgccaagcagaaggaac 131
DB 159 tacaacgcacagtggtgccaaggtgacagagttcttc-----gcacttggagcctaagac 212
QY 132 ctcccgctcagcgtctccatgaccccgctccttctgtgaagtcattcagaagccagc 191

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QY 192 gtgtgatcatgctcgtaagggccggcgccagctgaaccaacaatcgcgacgctcgca 251
Db 273 aaggtcatgctgtgtcaaggcttggaagtgcagtcgacgacttcattccagcagctgtgtg 332
QY 252 gctcaactggagcaggcgactgcattcgatgggggaagtggtacgaagaacag 311
Db 333 ccgctgcttccgcccgcgcatggtatcatcgtgtgcaactcggagatcaggaacaca 392
QY 312 gagaggaagggaagcccatggaaggagcgccctnctgtatcttggcatgtgtctct 371
Db 393 tctcgccgctgtagcagagtagccaacttgccctgctcttcgtagtccgcgtgagc 452
QY 372 ggaggaaggagggtgcccgaacggcccgctcctgtatg 410
Db 453 ggtggcgaaggaggcccgccacggaaccctcgctgagt 491
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Search completed: July 3, 2002, 07:56:21
Job time: 24336 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 3, 2002, 07:41:01 ; Search time 185.98 Seconds

(without alignments)
541,508 Million cell updates/sec

Title: US-09-300-482-14

Perfect score: 410
1 cccacgcgtccgcggtcatg.....gcacgcgcgtcttcatg 410

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 38353 segs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56.4	13.8	2087	4 US-09-058-692-1	Sequence 1, Appl
2	56.4	13.8	2087	4 US-09-584-628-1	Sequence 1, Appl
3	37.4	9.1	1524	2 US-08-716-942-24	Sequence 24, Appl
4	35.6	8.7	11958	4 US-09-134-246-8	Sequence 8, Appl
5	35.6	8.7	939	4 US-09-105-390-45	Sequence 45, Appl
6	35.6	8.7	1020	4 US-09-105-390-61	Sequence 61, Appl
7	35.6	8.7	2612	4 US-09-105-390-7	Sequence 7, Appl
8	35.6	8.7	8051	2 US-08-576-626A-2	Sequence 2, Appl
9	35.2	8.6	2990	1 US-08-572-951-1	Sequence 1, Appl
10	35.2	8.6	3476	3 US-08-630-916A-47	Sequence 47, Appl
11	35	8.5	2830	2 US-09-010-928B-1	Sequence 1, Appl
12	34.4	8.4	2277	1 US-08-676-967-5	Sequence 5, Appl
13	34.4	8.4	2277	1 US-08-676-974-5	Sequence 5, Appl
14	34.4	8.4	2277	2 US-09-098-487-5	Sequence 5, Appl
15	34	8.3	2713	3 US-08-804-439A-13	Sequence 13, Appl
16	34	8.3	2713	3 US-08-720-229-13	Sequence 13, Appl
17	34	8.3	3472	6 5244792-2	Patent No. 5244792
18	34	8.3	5020	3 US-08-938-291A-3	Sequence 3, Appl
19	33.8	8.2	1910	5 PCT-US92-05532-1	Sequence 1, Appl
20	33.8	8.2	2261	1 US-08-272-882B-1	Sequence 1, Appl
21	33.8	8.2	7218	1 US-08-232-463-14	Sequence 14, Appl
22	33.2	8.1	2040	2 US-08-533-669A-5	Sequence 5, Appl
23	33	8.0	1586	4 US-09-392-772-3	Sequence 3, Appl
24	33	8.0	49272	1 US-08-614-770A-1	Sequence 1, Appl
25	32.8	8.0	1312	1 US-08-205-506A-1	Sequence 1, Appl
26	32.8	8.0	1312	5 PCT-US94-02389-1	Sequence 1, Appl
27	32.8	8.0	3318	4 US-09-593-589-3	Sequence 3, Appl

28	32.4	7.9	28804	2 US-08-592-874-1	Sequence 1, Appl
29	32.4	7.9	28804	3 US-09-096-942-2	Sequence 2, Appl
30	32.4	7.9	28804	3 US-09-096-967-2	Sequence 2, Appl
31	32.2	7.9	720	4 US-09-459-956-1	Sequence 1, Appl
32	32.2	7.9	1929	2 US-08-818-253-1	Sequence 1, Appl
33	32.2	7.9	1929	2 US-08-818-253-5	Sequence 5, Appl
34	32.2	7.9	1929	4 US-08-818-252-1	Sequence 1, Appl
35	32.2	7.9	1929	4 US-08-818-252-5	Sequence 5, Appl
36	32.2	7.9	1959	2 US-08-818-253-3	Sequence 3, Appl
37	32.2	7.9	1959	4 US-08-818-252-3	Sequence 3, Appl
38	32.2	7.9	1971	2 US-08-818-253-7	Sequence 7, Appl
39	32.2	7.9	1971	4 US-08-818-252-7	Sequence 7, Appl
40	32.2	7.9	2680	2 US-08-533-306A-5	Sequence 5, Appl
41	32.2	7.9	2680	2 US-08-742-923A-5	Sequence 5, Appl
42	32.2	7.9	2887	2 US-08-533-306A-3	Sequence 3, Appl
43	32.2	7.9	2887	2 US-08-742-923A-3	Sequence 3, Appl
44	32	7.8	720	3 US-09-094-359-5	Sequence 5, Appl
45	32	7.8	720	3 US-09-094-359-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-09-058-692-1
Sequence 1, Application US/09058692
Patent No. 6162618
GENERAL INFORMATION:
APPLICANT: Warren, Richard L.
TITLE OF INVENTION: 6-phosphogluconate dehydr
SEQUENCE OF INVENTION: 4
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,692
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: GM10140
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
TELEFAX: 215-994-2222
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2087 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-058-692-1

Query Match 13.8%; Score 56.4; DB 4; Length 2087;
Best Local Similarity 48.4%; Pred. No. 3.3e-06;
Matches 193; Conservative 0; Mismatches 197; Indels 9; Gaps 1;
OY 12 gcgcatggggcagaacctgcctcaacatgcagagaaggggtcccatctctgtg 71

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Db 44 GCGGTAAGGCGTCTACCTTGCCTTAATGATCWCCTGGTTACACAGTTGCTATC 103
Qy 72 tacacagagacaacctccaaggtgagacagacgcgcgctgcgaagcgcaagaaac 131
Db 104 TACAACCTGATGAAGAAAAGGAGATGTGATTCCTTCCATCTGAAAACAACTTT 163
Qy 132 ctcccgctctacgcgtccatcagccccgcgtccttctgtaagtcacatcagaagcagcg 191
Db 164 GTACCAAGCT-----ATGACGTTGAAGTTTGTGAACCTCAATGAAAACCTCTGT 214
Qy 192 gtggtgacatcgtcgtcgtcaagccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 251
Db 215 CGTATCATGCTGATGCTTCAAGCTGGACCTGTAACAGATGCTACTATCCAAAGCCCTTCTT 274
Qy 252 gctcacttgagagagagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 311
Db 275 CCACACCTTGACAAAGGATGATCTTGATTCACGCGWGAATTAATCTTCTTCAAAAGATACC 334
Qy 312 gagagagagagagagagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 371
Db 335 ATCCGTCGTATGAAGATTTGGCAACCTCWCCTGATCAACTTTATCGGTACTGCGTTTCT 394
Qy 372 gagagagagagagaggtgccccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 410
Db 395 GGTGTGAAAAAGGTGCCCTTGAAGGTCCTTCTATCATG 433

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RESULT 2
US-09-584-628-1
; Sequence 1, Application US/09584628
; Patent No. 6309866
; GENERAL INFORMATION:
; APPLICANT: Warren, Richard L.
; TITLE OF INVENTION: 6-phosphogluconate dehydr
; TITLE OF INVENTION: ogenase
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Decher, Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2793
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FASTSQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/584,628
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/058,692
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Falk, Stephen T
; REGISTRATION NUMBER: 36,795
; REFERENCE/DOCKET NUMBER: GM10140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-994-2488
; TELEFAX: 215-994-2222
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2087 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-584-628-1

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Query Match 13.8%; Score 56.4; DB 4; Length 2087;
Best Local Similarity 48.4%; Pred. No. 3..3e-06;
Matches 193; Conservative 0; Mismatches 197; Indels 9; Gaps 1;
Qy 12 gcggtcacttgagagagagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 71
Db 44 GCGGTAAGGCGTCTACCTTGCCTTAATGATCWCCTGGTTACACAGTTGCTATC 103
Qy 72 tacacagagacaacctccaaggtgagacagacgcgcgctgcgaagcgcaagaaac 131
Db 104 TACAACCTGATGAAGAAAAGGAGATGTGATTCCTTCCATCTGAAAACAACTTT 163
Qy 132 ctcccgctctacgcgtccatcagccccgcgtccttctgtaagtcacatcagaagcagcg 191
Db 164 GTACCAAGCT-----ATGACGTTGAAGTTTGTGAACCTCAATGAAAACCTCTGT 214
Qy 192 gtggtgacatcgtcgtcgtcaagccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 251
Db 215 CGTATCATGCTGATGCTTCAAGCTGGACCTGTAACAGATGCTACTATCCAAAGCCCTTCTT 274
Qy 252 gctcacttgagagagagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 311
Db 275 CCACACCTTGACAAAGGATGATCTTGATTCACGCGWGAATTAATCTTCTTCAAAAGATACC 334
Qy 312 gagagagagagagagagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 371
Db 335 ATCCGTCGTATGAAGATTTGGCAACCTCWCCTGATCAACTTTATCGGTACTGCGTTTCT 394
Qy 372 gagagagagagagaggtgccccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 410
Db 395 GGTGTGAAAAAGGTGCCCTTGAAGGTCCTTCTATCATG 433

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RESULT 3
US-08-716-942-24
; Sequence 24, Application US/08716942
; Patent No. 5849491
; GENERAL INFORMATION:
; APPLICANT: Terragen Diversity Inc.
; APPLICANT: Radomski, Christopher C. A.
; APPLICANT: Seow, Kah Tong
; APPLICANT: Warren, R. Anthony J.
; APPLICANT: Yap, Wei Ho
; TITLE OF INVENTION: METHOD FOR ISOLATING XYLANASE GENE
; TITLE OF INVENTION: SEQUENCES FROM SOIL DNA, COMPOSITIONS USEFUL IN SUCH METHOD
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Opedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/716,942
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/004,157
; FILING DATE: 20-Sep-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: TERR-P-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330

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1
TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1524
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: Internal
; ORIGINAL SOURCE:
; ORGANISM:
; FEATURE:
; NAME/KEY: sequence of xylanase gene identified by
; NAME/KEY: amplification of xylanase fragments from soil
US-08-716-942-24

Query Match          9.1%; Score 37.4; DB 2; Length 1524;
Best Local Similarity 50.6%; Pred. No. 0.34;
Matches 89; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 189 cgggtggtgatcatctgctcgaagcgcgccagttgaccagacatcggaagctc 248
DB 595 CCGCGAGTGGGAGCGGCTACATCGCCGACGCGCTGCGACCGCGACCGCCGACCC 654
QY 249 ggaagtcacttgagcaagcgactgcatcagatgagggagcaagtgatcagaagc 308
DB 655 AGTGGCCAGCTGTACATCAACAGCATCAGAGGGGAGGAGCCCAAGCAACGCC 714
QY 309 acggaagagagagagagagcgatgagagagcgcgccctcgtatcttgcatggg 364
DB 715 ATGTACAGCCTGTGTGACATCCTGCTGCGCGAGGGGGTCCGATCAACGCGGTGG 770

RESULT 4
US-09-134-246-8
; Sequence 8, Application US/09134246B
; Patent No. 6207377
; GENERAL INFORMATION:
; APPLICANT: Wayne, Jay
; TITLE OF INVENTION: Method For Construction Of Thermus-E. coli Shuttle
; TITLE OF INVENTION: Vectors And Identification Of Two Thermus Plasmid
; FILE REFERENCE: Thermus Shuttle Vector
; CURRENT APPLICATION NUMBER: US/09/134,246B
; CURRENT FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 8
; LENGTH: 11958
; TYPE: DNA
; ORGANISM: Thermus sp.
US-09-134-246-8

Query Match          8.7%; Score 35.8; DB 4; Length 11958;
Best Local Similarity 46.8%; Pred. No. 1.7;
Matches 152; Conservative 0; Mismatches 167; Indels 6; Gaps 1;
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QY 183 aagcacgggtgtgtatcatctgctcgaagcgccgagcgccagttgaccagaccatcgcg 242
DB 8139 aagcccttggtgctgtgagaaggtctccacaggggaggtgctgagagagaggaacccg 8198
QY 243 acgctgcagctcacttgtagcagagcgactgcatatctgaggggagagagtgatc 302
DB 8199 atggggggtcctgacctgagagagatcgccttcacagcgccgggtggaagatctcaag 8258
QY 303 gagaacacgagagagagaggaag 327
DB 8259 gagatgagaggaagagttcacgaaag 8283

RESULT 5
US-09-105-390-45/c
; Sequence 45, Application US/09105390
; Patent No. 6288303
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Raymond
; TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
; TITLE OF INVENTION: and Genes
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,390
; FILING DATE: Filed herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,675
; FILING DATE: 25-JUN-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Petithory, Joanne R.
; REGISTRATION NUMBER: P42,995
; REFERENCE/DOCKET NUMBER: 2000-0455.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX:
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 939 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..939
; OTHER INFORMATION:
US-09-105-390-45

Query Match          8.7%; Score 35.6; DB 4; Length 939;
Best Local Similarity 45.9%; Pred. No. 0.88;
Matches 119; Conservative 0; Mismatches 140; Indels 0; Gaps 0;
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Db	561	CCGAGAGCTGCACGCGCTGCTCGGGGTCCGCCCTACGCAAGTAGGGGTACACGTTACACAG	5020
OY	212	ggccggcgcgcgcagcttgaccagacatcgcgcgcctcgcagctcaacttggagcagggcga	2711
Db	501	CAGCGCGCGCCGCCCTGGACGGAGAGTAGGCACCAATGCGCCCACTGACGGCGACGGCC	4422
OY	272	ctgcatactgaatggggggaacgagctggtacagaaacacagagagggagagaagggcat	3311
Db	441	CTCCAGAAACCGCCCTTCGACGCGGGGTACGACACCCGACGACGAGCAGTGGGACGGC	3822
OY	332	ggagagcgcgcgcctcncg	350
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RESULT 6
US-09-105-390-61/c

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1 ? Sequence 61, Application US/09105390
2 ? Patent No. 6288303
3 ?
4 ? INFORMATION:
5 ?   APPLICANT: Rodriguez, Raymond
6 ?   TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
7 ?   TITLE OF INVENTION: and Genes
8 ?   NUMBER OF SEQUENCES: 66
9 ?   CORRESPONDENCE ADDRESS:
10 ?     ADDRESSEE: Delhinger & Associates
11 ?     STREET: 350 Cambridge Ave., Suite 250
12 ?     CITY: Palo Alto
13 ?     STATE: CA
14 ?     COUNTRY: USA
15 ?     ZIP: 94306
16 ?
17 ? COMPUTER READABLE FORM:
18 ?   MEDIUM TYPE: Diskette
19 ?   COMPUTER: IBM Compatible
20 ?   OPERATING SYSTEM: DOS
21 ?   SOFTWARE: FastSeq for Windows Version 2.0
22 ?   CURRENT APPLICATION DATA:
23 ?     APPLICATION NUMBER: US/09/105.390
24 ?     FILING DATE: Filed herewith
25 ?     CLASSIFICATION:
26 ?
27 ?   PRIOR APPLICATION DATA:
28 ?     APPLICATION NUMBER: 60/050.675
29 ?     FILING DATE: 25-JUN-97
30 ?
31 ?   ATTORNEY/AGENT INFORMATION:
32 ?     NAME: Pelichoroy, Joanne R.
33 ?     REGISTRATION NUMBER: P42,995
34 ?     REFERENCE/DOCKET NUMBER: 2000-0455.30
35 ?   TELECOMMUNICATION INFORMATION:
36 ?     TELEPHONE: 650-324-0880
37 ?     TELEFAX: 650-324-0960
38 ?     TELEX:
39 ?
40 ?   INFORMATION FOR SEQ ID NO: 61:
41 ?     SEQUENCE CHARACTERISTICS:
42 ?       LENGTH: 1020 base pairs
43 ?       TYPE: nucleic acid
44 ?       STRANDEDNESS: single
45 ?       TOPOLOGY: linear
46 ?
47 ?     FEATURE:
48 ?       NAME/KEY: Coding Sequence
49 ?       LOCATION: 1...1020
50 ?       OTHER INFORMATION:
51 ?
52 ? US-09-105-390-61

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Query Match	8.7%	Score 35.6;	DB 4;	Length 1020;
Best Local Similarity	45.9%;	Pred. No. 0.9;		
Matches 119;	Conservative 0;	Mismatches 140;	Indels 0.	Gaps 0.

[illegible]

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Qy	212	gagcgagcgagcgcaagttgtacagagacacatcgcgcagcgtcgcagctcaacttggacagcgca	27/17																																																																																																	
Db	582	CAGCGCGCGCGCCCTGTGGAGCGCAGGTAGCGCAGTATCGCGCCAGTACGGCGACGGCC	52/23																																																																																																	
Qy	272	ctgcatacaccgaatggggggaacagctggtaacagacagagagggagggaggaagggcat	33/11																																																																																																	
Db	522	CTCCGAGAACGCGCCCTCGGAGCGGGGTTAGAGACGCCGACACGACCTGTGGACGCC	46/3																																																																																																	
Qy	332	ggagagcgcgagcctctctg	350																																																																																																	
Db	462	GGTGTGACCGGGATCCG	444																																																																																																	

RESULT 7
US-09-105-390-7/c

```

1 Sequence 7, Application US/09105390
2 Patent No. 6288303
3
4 GENERAL INFORMATION:
5 APPLICANT: Rodriguez, Raymond
6 TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
7 TITLE OF INVENTION: and Genes
8 NUMBER OF SEQUENCES: 66
9 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: Dehlinger & Associates
11 STREET: 350 Cambridge Ave., Suite 250
12 CITY: Palo Alto
13 STATE: CA
14 COUNTRY: USA
15 ZIP: 94306
16
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Diskette
19 COMPUTER: IBM Compatible
20 OPERATING SYSTEM: DOS
21 SOFTWARE: FASTSEQ for Windows Version 2.0
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/09/105,390
24 FILING DATE: Filed herewith
25
26 CLASSIFICATION:
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: 60/050,675
29 FILING DATE: 25-JUN-97
30 ATTORNEY/AGENT INFORMATION:
31 NAME: Peltholy, Joanne R.
32 REGISTRATION NUMBER: P42,995
33 REFERENCE/DOCKET NUMBER: 2000-0455.30
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: 650-324-0880
36 TELEFAX: 650-324-0960
37
38 TELEX:
39
40 INFORMATION FOR SEQ ID NO: 7:
41 SEQUENCE CHARACTERISTICS:
42 LENGTH: 2612 base pairs
43 TYPE: nucleic acid
44 STRANDEDNESS: single
45 TOPOLOGY: linear
46
47 IS-09-105-390-7

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Query Match	8.7%;	Score 35.6;	DB 4;	Length 2612;
Best Local Similarity	45.9%;	Pred. No. 1.2;		
Matches 119;	Conservative 0;	Mismatches 140;	Indels 0;	Gaps 0;

[illegible]

Accession	Sequence	Position
Db	GCACACGGCGCGCAGCACCAGGCTGGAGACCTCCCGCGGCGCGCCCGTCCGCCACGGCGG	662
Qy	CGCGCAGTTGACCAAGACCATCGGAGCGCTCCGCGAGCTCACTTGGAGCAGGCGGACTGAT	277
Db	CGCGCCAGGCGCCCGCGCGGAGGAGGAGCACCAGCGCCCGCAGGCGCTCCGCAT	602
Qy	CATCGATCGGAGGGAAC	293
Db	TGCGGAGAGGCGCAGGC	586

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1  RESULT 10
2  US-08-630-916A-47
3  ; Sequence 47, Application US/08630916A
4  ; Patent No. 6011137
5  ;
6  ; GENERAL INFORMATION:
7  ; APPLICANT: Pirozzi, Gregorio
8  ; APPLICANT: Kay, Brian K.
9  ; APPLICANT: Fowlkes, Dana M.
10 ;
11 ; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
12 ; TITLE OF INVENTION: POLYPEPTIDES HAVING MW DOMAINS AND METHODS OF USING SAME
13 ;
14 ; NUMBER OF SEQUENCES: 124
15 ;
16 ; CORRESPONDENCE ADDRESS:
17 ; ADDRESSEE: Pennie & Edmonds
18 ; STREET: 1155 Avenue of the Americas
19 ; CITY: New York
20 ; STATE: New York
21 ;
22 ; COUNTRY: United States
23 ;
24 ; ZIP: 10036-2711
25 ;
26 ; COMPUTER READABLE FORM:
27 ; MEDIUM TYPE: Floppy disk
28 ; COMPUTER: IBM PC compatible
29 ; OPERATING SYSTEM: PC-DOS/MS-DOS
30 ; SOFTWARE: PatentIn release #1.0, Version #1.30
31 ;
32 ; CURRENT APPLICATION DATA:
33 ; APPLICATION NUMBER: US/08/630,916A
34 ; FILING DATE: 03-APR-1996
35 ; CLASSIFICATION: 435
36 ; ATTORNEY/AGENT INFORMATION:
37 ; NAME: MISROCK, S. LESLIE
38 ; REGISTRATION NUMBER: 18,872
39 ; REFERENCE/DOCKET NUMBER: 1101-203
40 ; TELECOMMUNICATION INFORMATION:
41 ; TELEPHONE: (212) 790-9090
42 ; TELEFAX: (212) 896-8864/9741
43 ; INFORMATION FOR SEQ ID NO: 47:
44 ; SEQUENCE CHARACTERISTICS:
45 ; LENGTH: 3476 bases
46 ; TYPE: nucleic acid
47 ; STRANDEDNESS: single
48 ; TOPOLOGY: linear
49 ;
50 ; MOLECULE TYPE: DNA
51 ;
52 ; US-08-630-916A-47

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Query Match	8.6%	Score 35.2	DB 3	Length 3476
Best Local Similarity	55.4%	Pred. No. 1.7		
Matches 67	Conservative 0	Mismatches 54	Indels 0	Gaps 0
QY 264	caggcgacatgcataatcgatggggggaacgagtgtagcgaagacacgagagggag	323		
Db 2143	CTGGGCAAGGTCACCCACCACGCTGAAGGAGCGCGAGACGATCCGGGTACGGAG	2202		
QY 324	aagcgacatggaggaacgcgcgcctnctgtatctctgtgcattggggtgtctctggaggaagag	383		
Db 2203	GAGAACGAAGGAAGATACATCATCTGCTGCTGACTGGCGTTTACCCGAGCGCTGGAA	2262		
QY 384	g 384			
Db 2263	G 2263			

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US-09-010-928B-1
: Sequence 1, Application US/09010928B
: Patent No. 5994099
: GENERAL INFORMATION:
: APPLICANT: Lewis, Randolph V
: APPLICANT: Hayashi, Cheryl Y
: TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
: TITLE OF INVENTION: CODING THEREFOR
: NUMBER OF SEQUENCES: 29
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
: STREET: 9110 GATEHOUSE RD. SUITE 500E
: CITY: FALLS CHURCH
: STATE: VIRGINIA
: COUNTRY: UNITED STATES OF AMERICA
: Zip: 22042
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/010,928B
: FILING DATE: 22-Jan-1998
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Murphy Jr., Gerald M
: REGISTRATION NUMBER: 28977
: REFERENCE/DOCKET NUMBER: 1447-109P
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2830 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: not relevant
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: HYPOTHEICAL: NO
: FEATURE:
: NAME/KEY: -
: LOCATION: 1..2830
: OTHER INFORMATION: /note="Flagelliform DNA sequence
: OTHER INFORMATION: taken from the 5' region. The putative start codon is at
: OTHER INFORMATION: position 219"
: NAME/KEY: CDS
: LOCATION: 219..2830
US-09-010-928B-1

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Query Match	8.5%	Score 35	DB 2	Length 2830
Best Local Similarity	44.9%	Pred. No. 1.8	Mismatches 161	Indels 0
Matches 131	Conservative	0	Gaps 0	
QY	119	ggcagaagaacac	ctccgctctacgctctccatctgaccccgctccctctgttaagtcac	178
Db	900	GGAGGAAGTGAAC	CTTTCGACACAGAGTGGCTGGAGACCATACAGCCAGGTGAGCT	959
QY	179	tcagaagccacag	ggtggtatcatgtctgttaaggccggtccaggtgacacagcat	238
Db	960	GGACCTGGTGGT	GCAGGTGAGACCTATGATGACCAAGAGCTGTGAGACTGTGAGCGGA	1019
QY	239	cgcagcgtctgc	agctctcaacttggagcaaggcgacttgcatactgattggggaaacgattg	298
Db	1020	CCAGGAGGTTAC	GGACCTGGTGAGCCGACCCAGGAGGTTATGAGACCTGGTGAGACCCGA	1079
QY	299	gtacagaagaca	cggagaggaaggaagccaatgagagacgcgagacuncctatccttgg	358
Db	1080	CCAGGAGGTTAC	GGACCTGGTGAGCTGGACCCAGGAGGTTACGAGACTGTGTGAGACTGGG	1139
QY	359	catgggtctctc	tgtagaagaaggatgtgccgcagagcccgctcttgatg	410
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RESULT 12
US-08-676-967-5
; Sequence 5, Application US/08676967
; Patent No. 5747317
; GENERAL INFORMATION:
; APPLICANT: COLLINS, KATHLEEN
; TITLE OF INVENTION: Human Telomerase
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Science & Technology Law Group
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/676,967
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman Ph.D., Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UCB96-055
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415)343-4342
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2277 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-676-967-5

Query Match      8.4% Score 34.4; DB 1; Length 2277;
Best Local Similarity 47.5%; Pred. No. 2.4;
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Db 504 CAAGGCCCTGAAGGCAATGACATGAAGAGATCAAGGGCCGCGACCGTGGCGTGACTG 563

QY 101 gaccgtgcagcgtgcgaagcagaagaacccctccgtctacggtctcattgacccgc 160
   || || || || || || || || || || || || || || || || || || || ||
Db 564 GGCGGTGGCCAAAGGACAAAGTCAAGGACACCCAGAGCGGTGAGCGCCATCGCGAGGAGAA 623

QY 161 gtcccttgtgaagtcattcgaagcagcggtgtgtatcatgtctcgtcaagcgcgcc 220
   || || || || || || || || || || || || || || || || || || || ||
Db 624 GAGCCACG--AGAGCAAGCACACAGAGAGCGGTGAAGAGAGGCCCGCGAGGAGAGGA 680

QY 221 gccagttgacagaccatcgagcgtcgcagctcacttggagcaggcgagctgcatcat 280
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Db 681 CATGAGAGAGAGAGAGAGACGACGACGACGACGACGACGACGACGACGACGAGCGGTGT 740

QY 281 cgatgtggggaacagtggtacgagaaacagagagagagagaga 324
   || || || || || || || || || || || || || || || || || || || ||
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RESULT 13
US-08-676-974-5
; Sequence 5, Application US/08676974
; Patent No. 570422
; GENERAL INFORMATION:
; APPLICANT: COLLINS, KATHLEEN
```

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; TITLE OF INVENTION: Human Telomerase
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Science & Technology Law Group
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/676,974
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman Ph.D., Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UCB96-055
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415)343-4342
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2277 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-676-974-5

Query Match      8.4% Score 34.4; DB 1; Length 2277;
Best Local Similarity 47.5%; Pred. No. 2.4;
Matches 135; Conservative 0; Mismatches 146; Indels 3; Gaps 1;

QY 41 catgcagagaagaaggtcccatctctgtgtacacagagaacccccaagtgcagca 100
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Db 504 CAAGGCCCTGAAGGCAATGACATGAAGAGATCAAGGGCCGCGACCGTGGCGTGACTG 563

QY 101 gaccgtgcagcgtgcgaagcagaagaacccctccgtctacggtctcattgacccgc 160
   || || || || || || || || || || || || || || || || || || || ||
Db 564 GGCGGTGGCCAAAGGACAAAGTCAAGGACACCCAGAGCGGTGAGCGCCATCGCGAGGAGAA 623

QY 161 gtcccttgtgaagtcattcgaagcagcggtgtgtatcatgtctcgtcaagcgcgcc 220
   || || || || || || || || || || || || || || || || || || || ||
Db 624 GAGCCACG--AGAGCAAGCACACAGAGAGCGGTGAAGAGAGGCCCGCGAGGAGAGGA 680

QY 221 gccagttgacagaccatcgagcgtcgcagctcacttggagcaggcgagctgcatcat 280
   || || || || || || || || || || || || || || || || || || || ||
Db 681 CATGAGAGAGAGAGAGAGACGACGACGACGACGACGACGACGACGACGACGAGCGGTGT 740

QY 281 cgatgtggggaacagtggtacgagaaacagagagagagagaga 324
   || || || || || || || || || || || || || || || || || || || ||
Db 741 CGACGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGA 784

RESULT 14
US-09-098-487-5
; Sequence 5, Application US/09098487
; Patent No. 5917025
; GENERAL INFORMATION:
; APPLICANT: COLLINS, KATHLEEN
; TITLE OF INVENTION: Human Telomerase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Science & Technology Law Group
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 3, 2002, 07:56:21 ; Search time 796.36 Seconds

(without alignments)
493.713 Million cell updates/sec

Title: US-09-300-482-27

Perfect score: 229

Sequence: 1 cagacctattttctgtc.....ctcaattatgggagacaa 229

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 100%

Listing first 45 summaries

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23: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74.2	32.4	1753	21	Arabidopsis thaliana
2	59.2	25.9	369	21	Zea mays DNA fragm
3	58.6	25.6	466	21	Zea mays DNA fragm
4	57.4	25.1	483	21	Zea mays DNA fragm
5	55.8	24.4	477	21	Zea mays DNA fragm
6	50.8	22.2	1639	21	Arabidopsis thaliana
7	47.6	20.8	1639	21	Arabidopsis thaliana
8	33.6	14.7	1105	19	S. pneumoniae deri
9	33.2	14.5	2659	24	Mouse ischaemic co

10	32.4	14.1	490	22	AAK67424	Human immune/haema
11	32.4	14.1	910715	20	AAK20248	Borrelia burgdorfe
12	32	14.0	385	21	AAK19560	Human secreted pro
13	32	14.0	15914	22	AAK84889	Human immune/haema
14	31.6	13.8	7151	24	AAK70693	Alfalfa acetyl-CoA
15	31	13.5	311	21	AAK08430	Fusarium venenatum
16	30.8	13.4	273254	21	AAK81914	Chlamydia pneumonia
17	30.4	13.3	902	22	AAK194223	Human neuroblastom
18	30.4	13.3	1026	21	AAK51822	Staphylococcus aur
19	30.4	13.3	4924	23	ABL20684	Drosophila melanog
20	30.4	13.3	5116	23	ABL09500	Drosophila melanog
21	30.4	13.3	15249	18	AAK74413	Staphylococcus aur
22	30.2	13.2	450	22	ABA13950	Human nervous syst
23	30.2	13.2	740	22	AAK07506	Human CDNA clone (
24	29.8	13.0	2764	22	AAK42481	Human CDNA encodin
25	29.8	13.0	4434	20	AAK61678	B. burgdorferi ant
26	29.8	13.0	4485	20	AAK61677	B. burgdorferi ant
27	29.8	13.0	116277	20	AAK20249	Borrelia burgdorfe
28	29.6	12.9	364	23	AAK75577	DNA encoding novel
29	29.6	12.9	584	22	ABA63142	Human foetal liver
30	29.6	12.9	584	22	ABA30391	Probe #8857 for ge
31	29.6	12.9	584	22	AAK11574	Human brain expres
32	29.6	12.9	584	22	AAK37343	Human bone marrow
33	29.6	12.9	584	22	AAK18173	Probe #8106 for ge
34	29.6	12.9	584	22	AAK13188	Probe #11874 used
35	29.6	12.9	1435	17	AAK43709	Human inhibitor of
36	29.6	12.9	2580	23	AAK87959	DNA encoding novel
37	29.6	12.9	2580	18	AAK70838	Human apoptosis in
38	29.6	12.9	2589	18	AAK61590	Human c-IAP1. Hom
39	29.6	12.9	3516	22	AAK54169	S. epidermidis gen
40	29.6	12.9	3512	18	AAK72711	Human inhibitor of
41	29.6	12.9	3532	20	AAK22143	Human cellular inh
42	29.6	12.9	3732	19	AAK55040	Human HIRAP-2 codin
43	29.6	12.9	3773	22	AAK54437	S. epidermidis gen
44	29.6	12.9	5608	23	ABL13474	Drosophila melanog
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ALIGNMENTS

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KW	Protein identification; signal transduction pathway;
KW	metabolic pathway; promoter; termination sequence; ss.
OS	Arabidopsis thaliana.
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XX	DT	17-OCT-2000 (first entry)				
DE	Zea mays DNA fragment SEQ ID NO: 20807.					
XX	Hybridisation assay; genetic mapping; gene expression control;					
KW	protein identification; signal transduction pathway; metabolic;					
KW	pathway; promoter; termination sequence; corn; ss.					
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KW protein identification; signal transduction pathway;
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AC AAZ96449;
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DT 10-APR-2000 (first entry)
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KW Treatment; prevention; disease; diagnosis; gene therapy; screening;
XX bacterial; antimicrobial; antibiotic; pathogenesis; infection; ss.
XX
OS Streptococcus pneumoniae.
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PN WO9806734-A1.
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PD 19-FEB-1998.
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PF 15-AUG-1997; 97WO-US14436.
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PR 16-AUG-1996; 96OS-0024022.
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PA (SMK ) SMITHKLINE BEECHAM CORP.
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PI Black MT, Hodgson JE, Knowles DJC, Lometto MA, Nicholas RO;
PI Stodola RK;
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XX WPI, 1998-159452/14.
DR P-PSDB; AAY86134.
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XX Streptococcus pneumoniae proteins and related DNA - useful for
PT screening compounds for antibacterial activity
XX
XX Claim 4; Page 291; 640pp; English.
XX
XX This invention describes novel isolated Streptococcus pneumoniae
CC polynucleotides (see AAZ96173-296494) and their encoded proteins (see
CC AAY85792-Y86182). The DNA, vectors and host cells described in the
CC method of the invention are useful for the recombinant expression of the
CC polypeptides. The polypeptides are useful for treatment or prevention of
CC disease, or diagnosis of disease related to expression or activity of
CC such a polypeptide. They can also be used to screen for compounds which
CC interact with and inhibit or activate such a polypeptide. The
CC polypeptides (or DNA encoding them, via gene therapy) are also useful
CC for inducing an immunological response in a mammal. The antagonists are
CC particularly useful to identify antimicrobial compounds and antibiotics.
CC They are also useful to determine their role in pathogenesis of
CC infection, dysfunction and disease.
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DB 164 AAGGAAAGTGACAGAGAGAGAGAAA 141
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RESULT 9
ABI99829
ID ABI99829 standard; cDNA; 2659 BP.
XX
AC ABI99829;
XX
DT 07-MAR-2002 (first entry)
XX
DE Mouse ischemic condition related cDNA sequence SEQ ID NO:948.
XX
KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
XX vasospastic ischaemia; ischemic condition; ischemic disease; ss.
XX
OS Mus musculus.
XX
PN WO200188188-A2.
XX
PD 22-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-JP04192.
XX
PR 18-MAY-2000; 2000JP-0145977.
XX
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX
XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
PI
```


DR MPI: 2002-034733/04.
DR P-PSDB: ABB57340.
XX
PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
PT expression levels of particular genes defined in the specification or
PT by determining the expression profile of a gene group comprising these
PT genes -
XX
XX Claim 2: Page 2399+2403; 2690pp; English.
XX
XX The present invention describes a method for examining ischaemic
CC conditions, comprising measuring the expression levels of particular
CC genes (1) in a test sample or determining the expression profile of a
CC gene group in the sample comprising genes selected from (1). The method
CC is useful for examining the ischaemic condition (e.g. compressive
CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
CC expression levels of particular genes (ABI99202 to ABI99912, encoding
CC the protein sequences in ABB57020 to ABB57374) or by determining the
CC expression profile of a gene group comprising these genes. The
CC expression levels or expression profiles produced by these genes are
CC used as an indicator when screening for ischaemic condition-improving
CC drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914
CC represent PCR primers for a mouse ischaemic condition related sequence,
CC which are used in the exemplification of the present invention.
CC
XX
SQ Sequence 2659 BP; 634 A; 773 C; 544 G; 708 T; 0 other:

Query Match 14.5%; Score 33.2; DB 24; Length 2659;
Best Local Similarity 53.0%; Pred. No. 1.4;
Matches 71; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 5 ccttattttctgtcattgtcctcaattcagagagatgaattgcgtcaaccaca 64
DB 1922 cccaacttcattatgtacatcttaaaatgacacacatgagagaaagctaaacaac 1981
QY 65 acaagatagccttgctgctgattgctgttaaggcaaatctgcaccatattgct 124
DB 1982 aaaaaaaacatgtaagggtgagcattgaattgcttcattccatacatattgt 2041
QY 125 tgaagaaggctcc 138
DB 2042 gtaaacgatttc 2055

RESULT 10
AAK67424
ID AAK67424 standard; DNA; 490 BP.
XX
AC AAK67424;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SRQ ID NO:22236.
XX
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
XX WO200157182-A2.
PN
PD 09-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01354.
PF
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR

PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUL-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226581.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0234984.
PR 27-SEP-2000; 2000US-0235634.
PR 27-SEP-2000; 2000US-0235636.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR

PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249287.
PR 17-NOV-2000; 2000US-0249289.
PR 01-DEC-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 05-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI: 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis -
XX
XX
PS Disclosure: SEQ ID NO 22236; 3071pp + Sequence Listing; English.
XX
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and

CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 490 BP; 164 A; 75 C; 103 G; 148 T; 0 other;

Query Match 14.1%; Score 32.4; DB 22; Length 490;
Best Local Similarity 64.9%; Pred.No.1.4;
Matches 48; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 40 agattaattatgcgtcaacccacacaaagatagagcttgctggtatgctgttaatgg 99
Db 402 aaaaaattatgagcatgcattacccaatgaagctgagctggaaggggtccatgg 461
QY 100 gcaaatctggcgc 113
Db 462 gctaaatctgggac 475

RESULT 11
AAK20248/C
ID AAK20248 standard; DNA; 910715 BP.
XX
AC AAK20248;
XX
DT 04-MAY-1999 (first entry)
XX
XX Borrelia burgdorferi polynucleotide sequence #1.
DE
XX
XX Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease;
KW epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;
KW infection; diagnosis; characterisation; detection; ds.
OS
XX
XX Borrelia burgdorferi.
PN
XX
XX WO9858943-A1.
XX
XX
XX 30-DEC-1998.
XX
XX
XX 18-JUN-1998; 98WO-US12764.
XX
XX
XX 03-SEP-1997; 97US-0057483.
XX
XX 20-JUN-1997; 97US-0050359.
XX
XX 22-JUL-1997; 97US-0053344.
XX
XX 22-JUL-1997; 97US-0053377.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX (MEDI-) MEDIMUNE INC.
XX
XX Clayton R, Dougherty BA, Fraser C, Lathigra R, Smith HO;
XX
XX White OR;
XX
XX WPI: 1999-081217/07.
XX
XX
XX New isolated Borrelia burgdorferi nucleic acids - used to develop
XX products for the detection, diagnosis, characterisation, prevention
XX and therapy of infections, particularly Lyme disease
XX
XX
PS Claim 1; Page 157-671; 1128pp; English.
XX
XX
CC AAK20248 to AAK20402 represent polynucleotide sequences isolated from
CC Borrelia burgdorferi (Bb). Products derived from Bb can be used for

08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
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PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249266.
PR 17-NOV-2000; 2000US-0249267.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;
WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
useful for preventing, diagnosing and/or treating cancers and
metastasis -

PS Disclosure; SEQ ID NO 39701; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytosolic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (II), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87894 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.

Sequence 15914 BP; 5450 A; 2843 C;2872 G; 4749 T; 0 other;

Query Match	14.0%;	Score 32;	DB 22;	Length 15914;
Best Local Similarity	52.2%;	Pred. No. 6.5;		
Matches	71;	Conservative	0;	Mismatches 65;
			Indels	0;
			Cane	0;

Oy	54	ctcaaccacacaaagaatagcttgccttgatgtgcctgtaagcgttaagcggcaaatctggcac	113
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Oy	114	tcaatattgcttgaagaaggcttcccaattccggttcaacacggacacattccaag	171
Db	5867	tttcaattatgcacaactcgtgagaagcgttltcaagttgacaaaggaccttlttgaag	5924
RESULT 15			
ID	AAF08430	standard; cDNA; 311 BP.	
AC	AAF08430;		
DT	13-MAR-2001	(first entry)	
DE	Fusarium venenatum EST SEQ ID NO:953.		
XX			
KW	Multiple gene expression; filamentous fungal cell; EST;		
KW	expressed sequence tag; Fusarium venenatum; Aspergillus niger;		
KW	Aspergillus oryzae; Trichoderma reesei; identification; recombination;		
KW	culture condition; environmental stress; spore morphogenesis;		
KW	metabolic pathway engineering; catabolic pathway engineering; ss.		
XX			
OS	Fusarium venenatum.		
PN	WO200056762-A2.		
PD	28-SEP-2000.		
XX			
PF	22-MAR-2000; 2000WO-US07781.		
XX			
PR	22-MAR-1999; 99US-0273623.		
PA	(NOVO) NOVO NORDISK BIOTECH INC.		
PA	(NOVO) NOVO NORDISK AS.		
PI	Berka RM, Rey MW, Shuster JR, Kaupinen S, Clausen IG, Olsen PB;		
DR	WPI; 2000-594572/56.		
XX			
XX			
PT	Monitoring differential expression of genes in filamentous fungal cells		
PT	uses fluorescence-labeled nucleic acids isolated from the cells and a		
PT	substrate of expressed sequence tags -		
PS	Claim 86; Page 746; 3161pp; English.		
CC	The present invention describes a method for monitoring differential		
CC	expression of genes in a first filamentous fungal (FF) cell relative to		
CC	expression of the same genes in one or more second filamentous fungal		
CC	cells. The method uses fluorescence-labeled nucleic acids isolated from		
CC	the FF cells and a substrate of expressed sequence tags (EST). The ESTs		
CC	are used in the methods for monitoring differential expression of genes		
CC	in a first filamentous fungal (FF) cell relative to expression of the		
CC	same genes in one or more second filamentous fungal cells. Monitoring		
CC	the global expression of genes from FF cells allows the production		
CC	potential of the microorganisms to be improved. New genes may be		
CC	discovered, possible functions of unknown open reading frames can be		
CC	identified and gene copy number variation and stability can be		
CC	monitored. The expression of genes can be used to study how FF cells		
CC	adapt to changes in culture conditions, environmental stress, spore		
CC	morphogenesis, recombination, metabolic or catabolic pathway		
CC	engineering. Using ESTs provides several advantages over genomic or		
CC	random cDNA clones including elimination of redundancy as one spot on an		
CC	array equals one gene or open reading frame, and organisation of the		
CC	microarrays based on function of the gene products to facilitate		
CC	analysis of the results. AAF07478 to AAF11247 represents ESTs from		
CC	Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus		
CC	niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and		
CC	AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are		
CC	all specifically claimed in the present invention.		

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OM nucleic - nucleic search, using sw model

Run on: July 3, 2002, 07:41:08 ; Search time 185.98 seconds
(without alignments)
302.452 Million cell updates/sec

Title: US-09-300-482-27

Perfect score: 229

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Scoring table:

IDENTITY-NUC
Gapop 10.0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/backfilest1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30.4	13.3	1026	US-09-149-624-1	Sequence 1, Appl
2	29.6	12.9	1435	PCT-US95-05922A-1	Sequence 1, Appl
3	29.6	12.9	2580	US-08-511-485-7	Sequence 7, Appl
4	29.6	12.9	2589	US-08-569-749-1	Sequence 1, Appl
5	29.6	12.9	2589	PCT-US96-12860-1	Sequence 1, Appl
6	29.6	12.9	3532	US-09-205-204-1	Sequence 1, Appl
7	29.6	12.9	3732	US-08-212-971-7	Sequence 7, Appl
8	29.6	12.9	3732	US-08-800-929A-7	Sequence 7, Appl
9	29.6	12.9	3732	US-09-617-053A-7	Sequence 7, Appl
10	29.6	12.9	72604	US-09-268-992-7	Sequence 7, Appl
11	28.8	12.6	618	US-09-385-982-59	Sequence 59, Appl
12	28.4	12.4	270	US-08-589-080-3	Sequence 3, Appl
13	28.4	12.4	1629	US-08-589-080-2	Sequence 2, Appl
14	27.4	12.0	964	US-08-755-587-23	Sequence 23, Appl
15	27.4	12.0	1041	US-08-755-587-22	Sequence 22, Appl
16	27.4	12.0	1050	US-08-755-587-21	Sequence 21, Appl
17	27.4	12.0	1521	US-08-913-462-37	Sequence 37, Appl
18	27.4	12.0	1599	US-08-737-336-5	Sequence 5, Appl
19	27.4	12.0	6203	US-09-134-218-3	Sequence 3, Appl
20	27.4	12.0	8010	US-09-521-526-2	Sequence 2, Appl
21	27.4	12.0	8010	PCT-US95-11859-2	Sequence 2, Appl
22	27.4	11.8	756	US-08-530-165-1	Sequence 1, Appl
23	27.4	11.8	1008	US-07-904-073-1	Sequence 1, Appl
24	27.4	11.8	1008	US-07-904-071-1	Sequence 1, Appl
25	27.4	11.8	1770	US-08-381-603-1	Sequence 1, Appl
26	27.4	11.8	1770	US-08-924-376-1	Sequence 1, Appl
27	27.4	11.8	1770	US-08-685-212-1	Sequence 1, Appl

28	27	11.8	1770	5	PCT-US94-02414-1	Sequence 1, Appl
29	27	11.8	1770	5	PCT-US96-08899-1	Sequence 1, Appl
30	27	11.8	3011	1	US-07-821-716-1	Sequence 1, Appl
31	26.8	11.7	801	4	US-09-276-531-111	Sequence 11, App
32	26.6	11.6	714	3	US-08-643-704A-44	Sequence 44, Appl
33	26.6	11.6	773	4	US-09-227-357-47	Sequence 47, Appl
34	26.6	11.6	816	3	US-08-643-704A-47	Sequence 47, Appl
35	26.6	11.6	900	3	US-08-643-704A-46	Sequence 46, Appl
36	26.6	11.6	1236	3	US-08-643-704A-48	Sequence 48, Appl
37	26.6	11.6	2854	4	US-08-936-165A-66	Sequence 66, Appl
38	26.6	11.6	4649	6	5183745-1	Patent No. 5183745
39	26.6	11.6	5118	4	US-08-669-785-3	Sequence 3, Appl
40	26.6	11.6	6441	4	US-08-669-785-1	Sequence 1, Appl
41	26.6	11.6	6443	6	5183745-5	Patent No. 5183745
42	26.6	11.6	9432	1	US-08-277-231A-1	Sequence 1, Appl
43	26.6	11.6	9432	2	US-08-473-750-4	Sequence 4, Appl
44	26.6	11.6	9432	2	US-08-477-326-4	Sequence 4, Appl
45	26.6	11.6	17041	1	US-08-076-011-1	Sequence 1, Appl

ALIGNMENTS

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RESULT 1
US-09-149-624-1
; Sequence 1, Application US/09149624
; Patent No. 6222026
; GENERAL INFORMATION:
; APPLICANT: Palmer, Leslie M.
; APPLICANT: Kosmatka, Anna L.
; APPLICANT: Trainin, Christopher M.
; APPLICANT: Warren, Richard L.
; TITLE OF INVENTION: gcp
; FILE REFERENCE: GM10166
; CURRENT APPLICATION NUMBER: US/09/149,624
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1023)
US-09-149-624-1

Query Match      13.3%; Score 30.4; DB 4; Length 1026;
Best Local Similarity 52.3%; Pred. No. 0.46;
Matches 67; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 32 attcaggaataatgctgctcaaccacacagaataagctctgattgct 91
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Db 886 attccagtcctaatatgacagataatgctgcaatgattgctgcccacat 945

QY 92 gttaatggcgaataatgctgctcaaccacacagaataagctctgattgct 151
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Db 946 gttaatggcgaataatgctgctgattgattgattgattgattgattgatt 1005

QY 152 caacggaa 159
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Db 1006 gaagagta 1013

RESULT 2
PCT-US95-05922A-1
; Sequence 1, Application PC/TUS9505922A
; GENERAL INFORMATION:
; APPLICANT: HE, ET AL.
; TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:

```

```

ADDRESS: CARELLA, BYRN, BAIN, GILFILLAN,
ADDRESS: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05922A
FILING DATE: 11 MAY 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-292
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1435 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
PCT-US95-05922A-1

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Query Match	Similarity	12.9%	Score 29.6	DB 5	Length 1435
Best Local	Similarity 47.8%		Pred. No. 1		
Matches	86	Conservative	0	Mismatches 94	Indels 0
				Gaps	0
QY	8	tattttctctgcatttcgcttccaatttcgaagaattatctgcgtcacaaccaaca	67		
Db	1238	TAGTATGCCAGGAAATGTGCCCCCTCTCTNAGAAATGCCCTATTTCGAGGCTATATATA	1297		
QY	68	agaataagcccttgcgtgattgcgtcttaatgaggcaaatctcggcaatcataatgcttga	127		
Db	1298	AGGGTACGTTCGTGCATATTTCTCTTAAAGAAATAATGTATATTTTAACTGCATTA	1357		
QY	128	aaagggtccccaatccgcgttaaacaagaacacattccaaaggtatattgaggcataaga	187		
Db	1358	AAAGTCTTTAAATATATGTGTAACACTTTGAAGCATCTTAAATGAAGAAGGAAATTATA	1417		

RESULT 3
US-08-511-485-7
Sequence No. 7, Application US/08511485
Patent No. 5919912
GENERAL INFORMATION:
APPLICANT: Korneljuk, Robert G.
APPLICANT: Mckenzie, Alexander E.
APPLICANT: Bald, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200134
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2580 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: DNA (genomic)
US-08-511,485-7

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Query Match	12.9%	Score 29.6	DB 2	Length 2580
Best Local Similarity	47.8%	Pred. No. 1.3		
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				Indels 0
				Gaps 0
QY	8	tatttttctgcatctgtgtcctaattcagagagataataatgcgtcaaccacaca	67	
Db	2006	TAGATGCCAGGAATGTGCCCTTCTCTAAGAAATGCCCATTTTGGAGGGATATATCA	2065	
QY	68	agaaatggccttgcgtgattgcgtcttaatggtgcacaaatctgcacatcaatattgcttga	127	
Db	2006	AGGGTACTGTCTTACATTTCCTCTTAAGAAAAATAGTCTATATTATTAACTGCATTA	2125	
QY	128	aaaggcttcaccatccggttaaacaaggacacatttccaaagtcttatgtggccaataga	187	
Db	2126	AAAGGCTTTAAATATTCTTTGACACACTTGAAGCCACTCTAATGAATAAAGGAATTATGA	2185	

RESULT 4
 US-08-569-749-1
 ; Sequence 1, Application US/08569749
 Patent No. 6187557
 GENERAL INFORMATION:
 APPLICANT: Roche, Mike
 APPLICANT: Goeddel, David V
 TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
 STREET: 4 Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 Zip: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/569,749
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Brezner, David J.
 REGISTRATION NUMBER: 24,774
 REFERENCE/DOCKET NUMBER: A-62464/DJB
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989

TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2589 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-569-749-1

Query Match 12.9%; Score 29.6; DB 4; Length 2589;
Best Local Similarity 47.8%; Pred. No. 1.3;
Matches 86; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 8 tatttttctgtcattgtctcaaatcaggagatlaattgctcgaaccacaaca 67
DB 1963 TACTATGCCAGGAATGTGCCCTTCTCTAAGAAAATGCCCTATTTCAGGGGTATATCA 2022
QY 68 agaataggccttgcgtgattgctgttaatgggcaaatctgcactcaatatgttga 127
DB 2023 AGGCTACTGTCTGCTACATTTCTCTTAAAGAAAATAGCTATATTTTAACTGCATFA 2082
QY 128 aaagggtccccaattccggttaacaacggaaccattccaaggttatgggcataaga 187
DB 2083 AAAGCTTTAAATTTGTTGAACACTTGAAGCCATTAAGTAAAGGAATTATGA 2142

RESULT 5
PCT-US96-12860-1

; Sequence 1, Application PC/TUS9612860
; GENERAL INFORMATION:
; APPLICANT: TULARIK, INC.
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/12860
; FILING DATE: 06 AUG 1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DUB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2589 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US96-12860-1

Query Match 12.9%; Score 29.6; DB 5; Length 2589;
Best Local Similarity 47.8%; Pred. No. 1.3;

Matches 86; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 8 tatttttctgtcattgtctcaaatcaggagatlaattgctcgaaccacaaca 67
DB 1963 TACTATGCCAGGAATGTGCCCTTCTCTAAGAAAATGCCCTATTTCAGGGGTATATCA 2022
QY 68 agaataggccttgcgtgattgctgttaatgggcaaatctgcactcaatatgttga 127
DB 2023 AGGCTACTGTCTGCTACATTTCTCTTAAAGAAAATAGCTATATTTTAACTGCATFA 2082
QY 128 aaagggtccccaattccggttaacaacggaaccattccaaggttatgggcataaga 187
DB 2083 AAAGCTTTAAATTTGTTGAACACTTGAAGCCATTAAGTAAAGGAATTATGA 2142

RESULT 6

US-09-205-204-1
; Sequence 1, Application US/09205204
; Patent No. 5958772
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-1 EXPR
; FILE REFERENCE: RTS-0020
; CURRENT APPLICATION NUMBER: US/09/205,204
; CURRENT FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 3532
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1160)..(3016)
US-09-205-204-1

Query Match 12.9%; Score 29.6; DB 2; Length 3532;
Best Local Similarity 47.8%; Pred. No. 1.5;
Matches 86; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 8 tatttttctgtcattgtctcaaatcaggagatlaattgctcgaaccacaaca 67
DB 2928 tagtagccaggaatgtgccctctctaagaaatgcccatttgcagggtataatca 2987
QY 68 agaataggccttgcgtgattgctgttaatgggcaaatctgcactcaatatgttga 127
DB 2988 agggtagcttgcgtacatttctcttaagaaaatagctataatttaacctgcataa 3047
QY 128 aaagggtccccaattccggttaacaacggaaccattccaaggttatgggcataaga 187
DB 3048 aaaggctttaaataattgttgaacacttgaagcactcatctaagtaaaaggagattatga 3107

RESULT 7

US-09-212-971-7
; Sequence 7, Application US/09212971B
; Patent No. 6107041
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratl, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009002
; CURRENT APPLICATION NUMBER: US/09/212,971B
; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 60/017,354

STREET: 3110 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
City: Raleigh
STATE: NC
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/755,587
FILING DATE: 25-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9523959.6
FILING DATE: 23-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525555.0
FILING DATE: 14-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9617961.9
FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kenneth D Sibley
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405-135
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1041 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 503..541
FEATURE:
NAME/KEY: exon
LOCATION: 501..541
US-08-755-587-22

	Query Match	Best Local Similarity	Score	DB	Length
Matches	58;	Conservative	0;	Mismatches	51;
				Indels	0;
				Gaps	0

	Query	DB	Score	DB	Length
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			53.2%		
742	atagctttttttttttatagaaatgccctgacatgaaaggaattatttttttcattcacctc	683			
62	acaacaagaatagagccttcgtagattgcgtgctgtaattgggcaaatctcg	110			
682	tttatctacatttaacgctttactgaattggcctgataagcagcagaaatgctag	634			

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 3, 2002, 05:09:07 ; Search time 5254.53 Seconds
(without alignments)
1258.492 Million cell updates/sec

Title: US-09-300-482-225
Perfect score: 316
Sequence: 1 gataaggtgcgcacactgag.....gaatggaggagactctga 316

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_da.*
2: gb_htg.*
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6: gb_pat.*
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8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_y1.*
15: em_da.*
16: em_fun.*
17: em_hum.*
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30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_inv.*

pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

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C	3	100	31.6	922	8	AF370479	AF370479 Arabidops
C	4	78.4	24.8	89154	8	ATAC010797	ATAC010797 Arabidops
C	5	69.8	22.1	67712	8	AC022355	AC022355 Arabidops
C	6	68.4	21.6	5348	8	S77133	S77133 GRF1-genera
C	7	63	19.9	720	8	CNS01918	ALL11059 Botrytis
C	8	60.6	19.2	2913	8	ZMU29162	U29162 Zea mays c1
C	9	60.2	19.1	130843	8	AF464738	AF464738 Zea mays
C	10	57.8	18.3	424	11	G37533	G37533 SHGC-57943
C	11	54.8	17.3	1205	6	AX085734	AX085734 Sequence
C	12	54.8	17.3	1574	9	HSABJ4326	AJ224326 Homo sapi
C	13	54.8	17.3	1778	9	BC016764	BC016764 Homo sapi
C	14	54.8	17.3	2130	9	AK056028	AK056028 Homo sapi
C	15	54.8	17.3	2501	9	BC005148	BC005148 Homo sapi
C	16	54.4	17.2	178802	2	AL360001	AL360001 Homo sapi
C	17	53.8	17.0	10304	8	AF166527	AF166527 Zea mays
C	18	52.2	16.5	3846	8	AB031012	AB031012 Zea mays
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C	24	51.4	16.3	175285	3	AC008259	AC008259 Drosophill
C	25	51.4	16.3	184079	3	AC008258	AC008258 Drosophill
C	26	51.4	16.3	259764	3	AE003840	AE003840 Drosophill
C	27	50	15.8	1316	10	BC019126	BC019126 Mus muscu
C	28	50	15.8	2357	10	BC006953	BC006953 Mus muscu
C	29	49.4	15.6	2128	8	AF415029	AF415029 Zea mays
C	30	49.4	15.6	2263	8	AF415109	AF415109 Zea mays
C	31	49.4	15.6	2291	8	AF415063	AF415063 Zea mays
C	32	49.4	15.6	3231	8	AF415072	AF415072 Zea mays
C	33	49.4	15.6	3232	8	AF415080	AF415080 Zea mays
C	34	49.4	15.6	3271	8	AF415075	AF415075 Zea mays
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C	43	49	15.5	2291	8	AF415063	AF415063 Zea mays
C	44	49	15.5	3231	8	AF415072	AF415072 Zea mays
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ALIGNMENTS

RESULT 1	AF189365	930 bp	mRNA	linear	PLN 10-JAN-2000
LOCUS	AF189365	Oryza sativa D-ribulose-5-phosphate 3-epimerase mRNA, complete cds.			
DEFINITION	AF189365	Oryza sativa D-ribulose-5-phosphate 3-epimerase mRNA, complete cds.			
ACCESSION	AF189365.1	GI:6007802			
VERSION	AF189365.1	GI:6007802			
KEYWORDS					
SOURCE					
ORGANISM					
	Oryza sativa.				
	Oryza sativa.				
REFERENCE					
AUTHORS	Kopriya, S., Kopriyova, A. and Suss, K.H.				
TITLE	Identification, cloning, and properties of cytosolic D-ribulose-5-phosphate 3-epimerase from higher plants				
JOURNAL	J. Biol. Chem. 275 (2), 1294-1299 (2000)				
MEDLINE	20092904				
REFERENCE					
AUTHORS	2 (bases 1 to 930)				
TITLE	Kopriya, S., Kopriyova, A. and Suss, K.-H.				
JOURNAL	Submitted (20-SEP-1999) Institute of Forest Biology and Tree Physiology, Am Flughafen 17, Freiburg im Breisgau 79085, Germany				

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 /note="F4P13.26, predicted by genefinder"
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 /note="hypothetical protein"
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 CMAJSEIIGRTAPRERLVDIEKILKSVKSKSDQSKSTKRVSSNSSESRPSKS
 NKKSSYTPPAKEFNRFLVSIIRIKDGSAAKSPDQCTPRTPEPNKVTAFKLCFT
 OPSAALVYLAICVKGNEARGEILOGMDPEPBGSGGCEGGEGR"
 complement(join(<7108. .7719,7796. .8075,8138. .8302,
 8384. .8859,8940. .9140,9249. .9492,9578. .9748,
 10009. .>10304))
 /gene="F28J7.5"
 complement(<7108. .>10304)
 /gene="F28J7.5"
 /note="F4P13.27"
 complement(join(7108. .7719,7796. .8075,8138. .8302,
 8384. .8859,8940. .9140,9249. .9492,9578. .9748,10009. .>10304))
 /gene="F28J7.5"
 /note="unknown protein"
 /codon_start=1
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 /db_xref="GI:6091716"
 /translation="NRMDLITAIYVALVSYLADESGQAPRIHTLSEVCEQNTFDW
 QTVGLMHSLSKSGQPEPIITRLISCTDDQKTKRGMLATFEVPSRHPKTDWPA
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 CNDLVRLITKTRPELCKDYGGLAMHIDRLVLAFLMLSKTEDEVRODTAHMTNLGD
 IYKGMISIMSYGFGCAAGLKKHINDMLTIPGVPRGEVPEVLMVHYHSGPISGNA
 SSTKIDHEDHNDVYDCNRLPPEPRPYREKTIEMPDPSKRGGLISLSECMNTLNEGIL
 RHAENGCRRPKTKTILSFLSKSTMELTRPKLAPESVHILDPQHEPPPIDERKTIY
 KIHILSTECTTIFDMQIVGFWMHSFQSGQPCNITRLISCTDEALKNYVGHDIAPHY
 VPSMRSHRITGDWYPAINKPAAVVHMLHTNTIDAEEVYLLDADMILRGPIITPMEFAA
 RMRPVSTPEESLPSLFLFSYLIGCDMLDLRLHTRNEADQVGGYIMHIEDLRK
 FALMYLTKQEOVARDKEHYKELTGDIYSGMSISEMYGSPGCAENLHNSINKELMI
 YGVYPEPADVRFVHYHGEKVVGNHNSFPKAMRNNDILNKKMAKRPDPSAVHOT
 DNDLQNRDLSTIECCQKLEALFLVHKHRNCEPGESETEKISYKSKVYNITKQOG
 SDIEHSQDSSSEGEFSTLKLMLALMLISGVFLVMLVFTSRGCTTGKGIYR
 NKRRTSYNTGGLDK"
 complement(10410. .10481)
 tsc_feature

[illegible]

REFERENCE 2 (bases 1 to 67712)
AUTHORS Lin, X. and Kaul, S.
TITLE Direct Submission
JOURNAL Submitted (01-FEB-2000) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA, xlin@tigr.org
REFERENCE 3 (bases 1 to 67712)
AUTHORS Town, C.D. and Kaul, S.
TITLE Direct Submission
JOURNAL Submitted (19-JAN-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org
COMMENT On Jan 19, 2001 this sequence version replaced gi:12280840.
Address all correspondence to: atet@tigr.org

BAC clone F9N12 is from Arabidopsis thaliana chromosome 1
The orientation of the sequence is from SP6 to T7 end of the BAC
clone.

Genes were identified by a combination of several methods: Gene
prediction programs including Genscan+ (Chris Burge,
http://CCR-081.mt.edu/GENSCAN.html), GenemarkHm (Mark Borodovsky,
http://genemark.biology.gatech.edu/Genemark/), Glimmer4 (a variant
of Glimmer3, see Mihalea Perlea,
http://www.tigr.org/softlab/glimmerm.htm/glimmerm.html, and
GeneSplicer (Mihalea Perlea and Steven Salzberg, contact
mperlea@tigr.org), searches of the complete sequence against a
peptide database and the plant EST database at TIGR
(http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to
indicate the level of evidence for their annotation. Genes with
similarity to other proteins are named after the database hits.
Genes without significant peptide similarity but with EST
similarity are named as unknown proteins. Genes without protein
or EST similarity, that are predicted by more than two gene
prediction programs over most of their length are annotated as
hypothetical proteins. Genes encoding tRNAs are predicted by
tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).
Simple repeats are identified by RepeatMasker (Arian Smit,
http://ftp.genome.washington.edu/RM/RepeatMasker.html).

FEATURES

SOURCE

1. 67712
Location/Qualifiers

/organism="Arabidopsis thaliana"

/cultivar="Columbia"

/db_xref="taxon:3702"

/chromosome="1"

/clone="F9N12"

1. 12863

/note="overlap with BAC clone F2K11
[AC008047:88005..100867]."

1

/note="21552 nt beyond this point were not included in the
submitted sequence due to an overlap with another bac
[F2K11]"

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4969..5104,5177..5350,5443..>5622)

/gene="F9N12.1"

3453..5622

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/note="contains similarity to Flavin-containing
monooxygenase"

join(3469..4024,4432..4526,4569..4721,4795..4877,
4969..5104,5177..5350,5443..5622)

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/codon_start=1

/product="unknown protein: 3469-5622"

/protein_id="AAG52151.1"

/db_xref="GI:12324359"

/translation="MAPALSPTRSHHVAVIGAGPAGIYAARELRREHSHVVEKKO
VGCTWITVDEVEDPLSDPTTRSYHSSVYRSLRNGTRCTGTRDFFPVRSQSRD
RRRPSHGEVLATLAKFAKEFGIEWVFETEVAVASAEIGKRIESTEKKKY
RRDIYDAVVVNGHYVRLAQIPGISMPGKEMHSHNRYRPEFRDVLFIIDHNY
AVLIGNSSAEDISDIAVAKVAVACRSNPADPTIVTGYNINMTISMESVDEG
SVYVONCKTISVDITMCTGYKHPPFLDTNGIIVVDNNGPLKDVPEFAFMLS
FIGLPMOVLPPMFILOSMTAGVYSGRIPLSKEDMMLIKTPEYSTLENGCIPIKRYT
HRMGTOTFEYDNWMLASQCGSCTEMREKMLANGVREKAHPETTYRDMDDHHLVSEA
YDPSLIS"

/cds

gene

mRNA

CDS

mRNA

gene

CDS

gene

mRNA

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CDS

gene

mRNA

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mRNA	gene	complement(join(<17308, .18791,18891, .19026,19143, .>19199)) /gene="P9N12.5" complement(17308, .19199) /gene="P9N12.5" /note="similar to GB:AAD43616 from [Arabidopsis thaliana]" complement(join(17308, .18791,18891, .19026,19143, .19199)) /gene="P9N12.5" /codon_start=1 /product="unknown protein; 19199-17308" /protein_id="AAG52154.1" /db_xref="GI:13324362" /translation="MYHPRRRDLFVGISWGKDLKDDAIGLFGNWKSRPLPSIFE ENKLSAIAKMKKFDLVISLALCKMMKLGEPSTIVTSSILNFCGKRSKPLPSIFE DOMYMGPRDPTIFPTPLIHGLFHNKRNKVAALVDRVWGCOCPNIVTGYVNGIC KRGDIDLEFNLNKKMEAKITADVIYNTITDSICKRHNDANLNKEMETKIRN VVTYSLSICGSRWSDASOLISDMTEKINRNLYTFNALIDAEFKEGREAEAL HDDMKRISIDPDIPTYNLSLNGFCMHDRDLDAKOMFEFVWSKDCFPOLDIYNTLIGF CKSKVEDGETELFREMSHRGLVGDIVYTYTLLIGLFHDGDCDNAQKFKOMVSGVGP DIMYTSILLDGLCNNGKLEKALEVEDYMRKOESEIKLIDYITYTTEGMCKAGVDGMD LFCSLSILGKVPNNVYNTMTISGCSKRLOEAYALLKMKEDGPLEDSCGYNTLIRA HLRQGDKAASAEILIREMRSCEFVGDASTGYIVANMLDGRLDKSFMDLMS" join(<19198, .19534,19579, .>19943) /gene="P9N12.6" 19198, 19943 /gene="P9N12.6" /note="similar to unknown protein GB:AAF18697 from [Arabidopsis thaliana]" join(19198, 19534,19579, .19943) /gene="P9N12.6" /codon_start=1 /product="hypothetical protein; 19198-19943"	
CDS	gene	Query Match Best Local Similarity 22.1%; Score 69.8; DB 8; Length 67712; Matches 98; Conservative 0; Mismatches 47; Indels 0; Gaps 0;	
mRNA	gene	47 aggtgatgctgctgctgaagctcttaccacataagaagtcgagcgcatactgctgagcccaatt 106 Db 36575 AGGTGAGCGCGCGCTTAGGCCCTTCCAAATGATGATGACGACGCTGCACCTGGACCCAACT 36634	
mRNA	gene	107 gcatcgctgcctgaaagctctatattgctgcctgcgagaccagagacacatcatctgtgc 166 Db 36635 GATATGCTGCAGCAAGTTCAGTGTTGGAGCTCCGAACCTGGGAGACTATATCCCTTT 36694	
mRNA	gene	167 tgaagaagaagcgtgaagggctctca 191 Db 36695 TCGGGGCTTAGTGTTGAGAAACACA 36719	
LOCUS	RESULT 6	S77133 5348 bp DNA linear PLN 26-SEP-1995	
DEFINITION	LOCUS	GRI1-general regulatory factor [Zea mays, XL80, genomic, 5348 nt].	
ACCESSION	DEFINITION	S77133	
VERSION	ACCESSION	S77133.1 GI:998429	
KEYWORDS	VERSION		
SOURCE	KEYWORDS		
ORGANISM	SOURCE	Zea mays XL80. Zea mays Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC Clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 5348) De Velten,N.C. and Ferl,R.J. Two genes encoding GF14 (14-3-3) proteins in Zea mays. Structure, expression, and potential regulation by the G-box binding complex Plant Physiol. 106 (4), 1593-1604 (1994) 95148741	

REMARK Genbank staff at the National Library of Medicine created this entry [NCBI_gibbsq_164519] from the original journal article.

This sequence comes from Fig. 1.

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FEATURES             source
    source            1..5348
                        /organism="Zea mays"
                        /db_xref="taxon:4577"
mrna                  join(1491..2583,2671..2749,2876..2998,4387..4503,
                        4610..4668)
gene                  2177..4669
                        /gene="GRF1"
                        /note="general regulatory factor"
cds                   join(2177..2583,2671..2749,2876..2998,4387..4503,
                        4610..4669)
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                        /note="14-3-3 protein homolog; This sequence comes from
                        Fig. 5"
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                        /translation="MASNELREEENVYAKIAEQAEREEMEVMEVAKTVDSSELT
VEBRULSVATKKNVIGARRASWRITISLEQKEEGRNDRYTLIKIDRGKTELTETIK
CDGIIKLETLEHLPVSSTAPESKRVFLKKMGDYRYLAEPFKGARCKDAENMTWAVAKYA
AODIALAEPLPHEIRLGLANFSEVFYEIINSDFSDPRACSLAKQAFFDEAISELDTLSEEE
SYKDSLIMQLRLNRLTWTSDISEDPEEFIEAPRKRDSSSQ"
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BASE COUNT 1325 a 1169 c 1203 g 1651 t

ORIGIN

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Query Match          21.6%; Score 66.4; DB 8; Length 5348;
Best Local Similarity 87.2%; Pred. No. 1.7e-11;
Matches 75; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
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Oy 225 agtactccctcgcgtttttttatttcacgicgcggtttagttcaacaatgaactagcgagcgcg 284
| ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3413 AATTACTCCCTCGCTGTGTTTATTGTCACCTTTAGTTAAATAACTAGCGGGCG 3472
|| ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Oy 285 actgatattcagaatactgaggagagga 310
|| ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 3473 ACAATATTTCGAGANTGAGTAGTA 3498

RESULT 7

LOCUS	CNS01918	720 bp	mRNA	linear	PLN 02-SEP-1999
DEFINITION	Botrytis cinerea strain T4 CDNA library under conditions of nitrogen deprivation.				
ACCESSION	AL11059				
VERSION	AL11059.1	GI:5825679			
KEYWORDS	CDNA library; nitrogen deprivation.				
SOURCE	Botryotinia fuckelliana.				
ORGANISM	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomyces; Helotiales; Sclerotiniaceae; Botryotinia.				
REFERENCE	Bitton,F., levis,C., Fortin,D., Pradier,J.M. and Brygoo,Y.				
AUTHORS	Direct Submission				
TITLE	Submitted (01-SEP-1999)				
JOURNAL	Phytopathologie, INRA, route de St Cyr, 78026 Versailles, France				
REFERENCE	2 (bases 1 to 720) Genoscope.				
AUTHORS	Direct Submission				
TITLE	Submitted (01-SEP-1999)				
JOURNAL	CP 5706 91057 EXRY cedex - FRANCE (E-mail : segrif@genoscope.cns.fr				
COMMENT	- Web : www.genoscope.cns.fr) The cDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII vector.				

Location/Qualifiers

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source
1. .720
/organism="Botrytislntia fuckeliana"
/strain="T4"
/db_xref="taxon:40559"
/note="Genosope sequence ID : W62E091"

BASE COUNT      226 a      146 c      178 g      170 t

ORIGIN

Query Match      19.9%; Score 63; DB 8; Length 720;
Best Local Similarity 65.0%; Pred. No. 7.6e-10;
Matches 93; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

OY      3      taagtgcgacacactcgagaaagaagtacccttccttaacatagaggtgatgctct 62
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      578      TAAGTCCCGCAACACAGAAACGATACCACGACTCAATCGAAGTTGATGTGGATT 637

OY      63      aggtctccacacatagacgctgcgcacatctgcctggcgacatgcatcgctcgag 122
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      638      GGGTCTCGAACAATGTATCAACGCGCAGATGCTGGCCAAATGTATGTGTGCAAGCAG 697

OY      123      ctctatactggcgctgcgagc 145
          || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      698      TGCTGTTTGGAGCCAGGACC 720

RESULT      8
LOCUS      ZMU29162/c      2913 bp      DNA      linear      PLN 20-JUL-1995
DEFINITION      Zea mays clone Mub69 ubiquitin gene, complete cds.
ACCESSION      U29162
VERSION      U29162.1 GI:902585
KEYWORDS
SOURCE
maize.
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 2913)
Liu,L., Maillet,D.S., Frappier,J.R., Walden,D.B. and Atkinson,B.G.
Characterization, chromosomal mapping, and expression of different
polyubiquitin genes in tissues from control and heat-shocked maize
seedlings
Biochem. Cell Biol. 73 (1-2), 19-30 (1995)
95391284
2 (bases 1 to 2913)
Frappier,J.H.
Direct Submission
Submitted (14-JUN-1995) J. Roger H. Frappier, Zoology, University
of Western Ontario, University of Western Ontario, Rm 340 B6G
Bldg., London, Ontario N6A 2T2, Canada
Location/Qualifiers
1. .2913
/organism="Zea mays"
/strain="Oh43"
/db_xref="taxon:4577"
/chromosome="4"
/map="4L position 186"
/clone="MubG9"
/tissue-type="radicle"
/dev_stage="5-day-old radicles"
1025. .1034
/note="heat shock element"
1193. .1196
1225. .2370
/note="polyubiquitin containing 5 ubiquitin monomers"
/codon_start=1
/product="ubiquitin"
/protein_id="AAC49014.1"
/db_xref="GI:902586"
/translation="MQIFVKLTGTITTEVESSDTIDNWKAKIQEGIPDQQRIL
FAGQQLDEGRLLADYNIQESTLHLVRLRGWQIFVKTLGTITTEVESSDTIDN
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FEATURES	ORIGIN
misc_feature	1225..1452
misc_feature	1453..1680
misc_feature	1681..1908
misc_feature	1909..2136
misc_feature	2137..2370
polya_signal	2357..2562
polya_site	2577
BASE COUNT	690 a 635 c 691 g 897 t
ORIGIN	
Query Match	19.2%; Score 60.6; DB 8; Length 2913;
Best Local Similarity	83.1%; Pred. No. 6.36-09;
Matches 69; Conservative 0; Mismatches 14; Indels 0; Gaps 0;	
QY 228 actccctcgtttttttatctgcgggttttgatcaaacgaactagcgagcagct 287	
Db 1097 actccctcgtttttttatctgcgggttttgatcaaacgaactagcgagcagca 1038	
OY 288 gatattcgagaatgagaggagga 310	
Db 1037 aatatTCGAGAACGAGGTAATA 1015	
RESULT 9	
AF64738	130843 bp DNA linear PLN 22-JAN-2002
LOCUS	
DEFINITION	Zea mays cultivar B73 putative gag protein, putative gag-pol precursor, putative transposase, putative copia-type pol polyprotein, putative copia-like retrotransposon Hopscotch polyprotein, putative gag protein, putative pipol, putative putative pol protein, putative pol protein, putative gag protein, and teosinte branched1 protein genes, complete cds.
ACCESSION	AF64738
VERSION	AF64738.1 GI:18254408
KEYWORDS	
SOURCE	
ORGANISM	Zea mays. Zea mays. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 130843) Ramakrishna,W., Samiuel,P., Emberton,J., Bronzino,A., Doebley,J. and Bennetzel,J. Direct Submission Submitted (26-DEC-2001) Department of Biological Sciences, Purdue University, West Lafayette, IN 47907, USA 2 (bases 1 to 130843) Lilston,E., Young,S., Kovchok,S., Kelzer,G. and Messing,J. Direct Submission Submitted (26-DEC-2001) Rutgers, The State University of New Jersey, The Plant Genome Initiative at Rutgers - Waksman Institute, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA Location/Qualifiers 1..130843 /organism="Zea mays" /cultivar="B73" /db_xref="taxon:4577" /chromosome="10" /map="10L: 197.6 MU" /clone="ZMWB_0178A11" 2034..12197 /gene="Z17B11.1" /note="similar to maize gag protein GB:AF090447.2

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GGSSWILDSGCTNHTREKRMFSSYEKNODPORATTFEDGNGVTVFRSDSIAFKG
VLEBGLIYVDRALDTCLIAKTNMGLMHRALHVGKMLKILKGEHLIGLNVH
FEKDEKSQTOETELKFLRAONEFLKIKIRSDNGTEFNSQIEGLEEGIKHEF
SSPYPOONGVVERKNTILDMARMLDEBTPDMEFAVANTACVAINRYLHLILK
KTSYELLGKKPNISYFRRFGSKILLVKRKSFKFAKTEGFLGYPDRRAVRF
NKSGLVEVSCDVVDEFNGSOVEQVDLDENGDPAVALRNMISIDVCKESELFP
SAOQOPSSSTASPTONEDFAQVDEVDQANEPDODGIDGOGDANODKDEDEORP
PAPRVHQAIDQDHPVDITLGDTHKGVTRSRVAFCEHSEFVSSTIEPRHVEALDSD
WVAMQELNNEFTRNEVHLVPRNQNVTGRVNRKQDEHGVTRKARLVAAGYS
OVGELDEFEYAPARLESIRILAYATYHGFXYOMDVKAFLNGPIKEEYVQOP
GFEDSEYNNHYKSLKALYGGKQAPRAVYECRLDRLNGKRVGADYDPLFKLEND
LFVCOIYVNDIIFGSTNESTCEPFRIMTQCEPMSEMLINGEADYKOLCOEFTIS
OTKTYODLSFKGKDAKPIKTPMGTNCHLDITGKSKVDOKFHHIPSRRLSPRAIM
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Query Match 19.1%; Score 60.2; DB 8; Length 130843;
Best Local Similarity 79.8%; Pred. No. 1.7e-08;
Matches 71; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 223 aagtaactccctcggtttttttatcgcgcgtttagtccaacatgaaatagcga 282

DB 119955 AACTACTCCACTCTATCTCTTTTATTTGTCCGCTTTAGTTCAAAAAGAACTATCGGG 120014

QY 283 cgactgatatcgagaatgaggaagctac 311

DB 120015 CAACAATAATTTTGAGAACATAGTAGTAC 120043

RESULT 10
LOCUS G37533 424 bp DNA linear STS 31-MAR-1998
DEFINITION SHGC-57943 Human Homo sapiens STS genomic, sequence tagged site.
ACCESSION G37533
VERSION G37533.1 GI:2997184
KEYWORDS STS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 424)
AUTHORS Myers, R.M.
TITLE Human STS (1997)
JOURNAL Unpublished
COMMENT

Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu
Primer A: CATGACAGCAGACACTGGC
Primer B: TTGAGACACGAGTTCCATC
STS size: 232
PCR Profile:
Initial incubation: 95 degrees C for 10 minutes
Denaturation: 94 degrees C for 30 seconds
Annealing: 60 degrees C for 30 seconds
Polymerization: 72 degrees C for 23 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9700
Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Amplifyng Gold Polymerase: 0.07 units/uL
Total Vol: 5 uL
Buffer: MgCl2: 2.5 mM

FEATURES
source Prepared with primer pairs derived from W80360 -- UniGene.
1. 424
Location/Qualifiers

KCl: 50 mM
Tris-HCl: 10 mM
pH: 8.3

STSS
primer_bind 132..363
primer_bind 132..151
BASE COUNT 114 a 103 c 75 g 125 t 7 others
ORIGIN

Query Match 18.3%; Score 57.8; DB 11; Length 424;
Best Local Similarity 50.0%; Pred. No. 3.8e-08;
Matches 137; Conservative 0; Mismatches 137; Indels 0; Gaps 0;

QY 4 aagtgcgacacactgagaagaagtaacccttcctgacatagagtgatggtgcta 63

DB 375 AAGTTCACTGGTTGAGAGACCCAGTCCATCTTGATATAGAGGTGATGAGTA 316

QY 64 ggtcctcaacatagacagtgccgcatctgctgggccaatgcaatgctgctggaagc 123

DB 315 GGTCTGACACCTGCTCCATTAATGTGACAGAGCGAGNGCTAATGCTGTGCTGCACT 256

QY 124 tctatatggcgctgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 183

DB 255 GCTATTNTNGNGTGAAGACCCAGATCTGTGATCAATCTATTGAANAATGTTGCTCA 196

QY 184 ggcctcagaacaacaacgatttggttctgctgtaagtaactccctcggtttt 243

DB 195 GAAGCTGCTCAGAAAGCTTCTCTGATCGGTGAACCATTAAGNGCCAGTGTCTCTGT 136

QY 244 ttatattgcgcggtttagtgaacatgaacta 277

DB 135 CATTGAATCTCCCTTTACTGGAACACAGAAVTA 102

RESULT 11
LOCUS AX085734 1205 bp DNA linear PAT 09-MAR-2001
DEFINITION Sequence 12 from Patent W00112790.
ACCESSION AX085734
VERSION AX085734.1 GI:13275684
KEYWORDS

SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1205)
AUTHORS Bandman, O., Lu, D.A., Yue, H., Tran, B., Hillman, J.L., Baughn, M.R.,
Lal, P. and Tang, Y.T.
TITLE Isomerase proteins
JOURNAL Patent: WO 0112790-A 12 22-FEB-2001;
Incyte Genomics, Inc. (US)
FEATURES
source Location/Qualifiers
1. 1205
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Incyte ID No: 2481256CB1"

BASE COUNT 331 a 224 c 291 g 359 t
ORIGIN

Query Match 17.3%; Score 54.8; DB 6; Length 1205;
Best Local Similarity 50.0%; Pred. No. 4.7e-07;
Matches 137; Conservative 0; Mismatches 137; Indels 0; Gaps 0;


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QY 4 aaggtgcgcacactgaaagaagtaaccttcccttgacataaggttgaatggtgtccta 63
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 480 AAGGTCACACGTTGAGAGACCCAGTTCATCTTTGGATATAGAGGTCAGTGGTAGTA 539
QY 64 ggtcctcaacctaaagcgtgagccgcatctgctggggccaattgcatctgctgtgaagc 123
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 540 GGTCCTGACACCTGTCATTAATGTGCAGAGCAGGAGCATMACTGATGTGTGTGGCAGT 599
QY 124 tctatatgtgcgtcgagcccaaggagccatcatatctgtgtgaggaagcgtgcag 183
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 600 GCTATTATGAGGAGTGAAGACCCAGATCTGTGATCATCATATTAGAATACTTTGCTCA 659
QY 184 ggtctcgaacaacaaactgatttgggtgttctgtctgaagtaactccctccgttttt 243
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 660 GAAGCTGCTCAGAAAGCTTCTTGTGATCGGTGAACACATGAGGACCCAGTGTCTGT 719
QY 244 ttatctgcgcgtttagtctcaacatgaacta 277
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 720 CATGAATCTCCTTTACTGGAACAGGATA 753

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RESULT 12

```

HSAJ4326      1574 bp  mRNA  linear  PRI 14-MAR-2001
LOCUS         Homo sapiens mRNA for putative ribulose-5-phosphate-epimerase,
DEFINITION   partial cds.
ACCESSION    AJ224326
VERSION      AJ224326.1 GI:2894531
KEYWORDS     Ribulose-5-phosphate-epimerase.
SOURCE       human.
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

```

```

REFERENCE    1 (bases 1 to 1574)
AUTHORS      Stanchi,F., Bertocco,E., Toppo,S., Dioguardi,R., Simionati,B.,
              Canata,N., Zimbello,R., Lanfranchi,G., Lanfranchi,G. and Valle,G.
              Characterization of 16 novel human genes showing high similarity to
              yeast sequences
              Yeast 18 (1), 69-80 (2001)

```

```

JOURNAL      21064499
MEDLINE      2 (bases 1 to 1574)
REFERENCE    Stanchi,F.
AUTHORS      Direct Submission
TITLE        Submitted (12-FEB-1998) Stanchi F., CRIIB Biotechnology Centre,
              Universita di Padova, Via G. Colombo 3, 35121, ITALY
JOURNAL      Location/Qualifiers
FEATURES     source
              1..1574
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /clone="IMAGE clone 206790"
              /tissue_type="spleen"
              /tissue_type="spleen"
              /clone_lib="Soares fetal liver spleen INFLS"
              /dev_stage="20 week-post conception fetus"
              /lab_host="DH10B (ampicillin resistant)"
              <1..526
              /codon_start=2
              /product="ribulose-5-phosphate-epimerase"
              /protein_id="CAA11895.1"
              /db_xref="GI:2894532"
              /db_xref="SPTREMBL:O43767"
              /translation="ESLRKQLGDPPEDFHMWVSKPEQWVKPMVAVAGANQYFHLLEAT
              ENPGALIKDIRNGKKVGLAIKPGTSVEVLAWANOIDMALVMTVEPGGCKFMEDM
              MPKVHMLRTQPSLDIEVDGSGVPTVHKCAEAGANMIVSGSAIMRSEDPRSVINLLR
              NVCSAAOKRSLDR"

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BASE COUNT 494 a 256 c 328 g 496 t

ORIGIN

Query Match 17.3%; Score 54.8; DB 9; Length 1574;
 Best local Similarity 50.0%; Pred. No. 4.9e-07;
 Matches 137; Conservative 0; Mismatches 137; Indels 0; Gaps 0;

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QY 4 aaggtgcgcacactgaaagaagtaaccttcccttgacataaggttgaatggtgtccta 63
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 314 AAGGTCACACGTTGAGAGACCCAGTTCATCTTTGGATATAGAGGTCAGTGGTAGTA 373
QY 64 ggtcctcaacctaaagcgtgagccgcatctgctggggccaattgcatctgctgtgaagc 123
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 374 GGTCCTGACACCTGTCATTAATGTGCAGAGCAGGAGCATMACTGATGTGTGTGGCAGT 433
QY 124 tctatatgtgcgtcgagcccaaggagccatcatatctgtgtgaggaagcgtgcag 183
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 434 GCTATTATGAGGAGTGAAGACCCAGATCTGTGATCATCATATTAGAATACTTTGCTCA 493
QY 184 ggtcctcgaacaacaaactgatttgggtgttctgtctgaagtaactccctccgttttt 243
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 494 GAAGCTGCTCAGAAAGCTTCTTGTGATCGGTGAACACATGAGGACCCAGTGTCTGT 553
QY 244 ttatctgcgcgtttagtctcaacatgaacta 277
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Db 554 CATGAATCTCCTTTACTGGAACAGGATA 587

```

RESULT 13

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BC016764      1778 bp  mRNA  linear  PRI 09-NOV-2001
LOCUS         Homo sapiens, clone MGC:22637 IMAGE:4107315, mRNA, complete cds.
DEFINITION   BC016764
ACCESSION    BC016764
VERSION      BC016764.1 GI:16876981
KEYWORDS     MGC.
SOURCE       human.
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

```

```

REFERENCE    1 (bases 1 to 1778)
AUTHORS      Strausberg,R.
              Direct Submission
TITLE        Submitted (05-NOV-2001) National Institutes of Health, Mammalian
              Gene Collection (MGC), Cancer Genomics Office, National Cancer
              Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
              USA

```

REMARK
 COMMENT
 NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 contact: amadan@systemsbiology.org
 Anup Madan, Jessica Fahay, Erin Helton, Mark Kettelman, Anuradha
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 32 Row: C Column: 6
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Hexamer frequency ORF
 analysis, similarity but not identity to protein.
 Location/Qualifiers
 1..1778
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="MGC:22637 IMAGE:4107315"
 /tissue_type="bone marrow, acute myelogenous leukemia"
 /clone_lib="NIH_MGC_55"
 /lab_host="DH10B"
 /note="Vector: pDNR-LIB"
 35..721
 /codon_start=1
 /product="Unknown (protein for MGC:22637)"
 /protein_id="AAH16764.1"
 /db_xref="GI:16876982"
 /translation="MASGCKIRPSILNSDLANLGAECRLMDSGADYHLIDYMSCHFV
 PNITFGHPVESLRKQLGDPPEDFHMWVSKPEQWVKPMVAVAGANQYFHLLEATENPG

CDS


```
RESULT 2
US-09-328-111-388/C
; Sequence 388, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Dertl, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111
; CURRENT FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: US 60/088,801
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 388
; LENGTH: 667
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(667)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-388

Query Match      10.9%; Score 34.4; DB 4; Length 667;
Best Local Similarity 63.1%; Pred. No. 0.013;
Matches 53; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Oy 57 tggctagagccttcacacccatagacgtggcgcatctgctggggccaatgctgcgc 116
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 352 TgGTGcAGGcGTGcCAACAcTAgAGcAGTgGcGTGcTGTGcTGTGcGAACAGTCTT 293
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 117 tggagcctctatattcggcgcgcgc 140
    ||||| ||||| ||||| |||||
Db 292 TGGCAGCGCTTATCATGTGCTATGC 269

RESULT 3
US-09-056-226-1/c
; Sequence 1, Application US/09056226B
; Patent No. 6177614
; GENERAL INFORMATION:
; APPLICANT: Colasanti, Joseph J.
; APPLICANT: Sundaresan, Venkatesan
; TITLE OF INVENTION: Control of Floral Induction in Plants
; FILE REFERENCE: CSHL94-04A4
; CURRENT APPLICATION NUMBER: US/09/056,226B
; CURRENT FILING DATE: 1998-04-07
; EARLIER APPLICATION NUMBER: US 09/000,640
; EARLIER FILING DATE: 1997-12-30
; EARLIER APPLICATION NUMBER: US 08/804,104
; EARLIER FILING DATE: 1997-02-20
; EARLIER APPLICATION NUMBER: PCT/US96/03466
; EARLIER FILING DATE: 1996-03-15
; EARLIER APPLICATION NUMBER: US 08/406,186
; EARLIER FILING DATE: 1995-03-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
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LENGTH: 3693
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (241)...(329)
; OTHER INFORMATION: Intron
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (628)...(746)
; OTHER INFORMATION: Intron
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (921)...(2347)
; OTHER INFORMATION: Intron
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(3693)
; OTHER INFORMATION: n = A, T, C or G
US-09-056-226-1

Query Match      10.8%; Score 34; DB 4; Length 3693;
Best Local Similarity 74.1%; Pred. No. 0.046;
Matches 43; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
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Oy 235 ccglttttttattcgtcgctttagtcaacatagacgagcgaactgat 292
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1457 CCTTCTTTTATCAGTGGCATTTAGTTTAAATCAACAGGAGCATTAATAT 1400

RESULT 4
US-08-737-524B-26
; Sequence 26, Application US/08737524B
; Patent No. 5912414
; GENERAL INFORMATION:
; APPLICANT: CARL SAVERIO FALCO
; APPLICANT: DOMINICK ANTHONY GUIDA, JR.
; APPLICANT: MARY ELIZABETH HARNETT LOCKE
; TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS, CHIMERIC
; TITLE OF INVENTION: GENES AND METHODS FOR INCREASING
; TITLE OF INVENTION: THE METHIONINE CONTENT OF THE SEEDS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WINDOWS 95
; SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,524B
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: LYNN M. CHRISTENBURY
; REGISTRATION NUMBER: 30,971
; REFERENCE/DOCKET NUMBER: BB-1059-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-5481
; TELEFAX: 302-773-0164
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 26:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 3639 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-08-737-524B-26

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Query Match	10.7%;	Score 33.8;	DB 2;	Length 3639;
Best Local Similarity	68.1%;	Pred. NO. 0.054;		
Matches 62;	Conservative	0;	Mismatches 27;	Indels 2;
				Gaps 1;

QY 211 tgccttcgcgtaagtaactccctcgcgttttttattatccgtcggttttagttcaaca 270
| | | | | | | | | | | | | | | | | | |
Db 55 TATTAGTGGATTAATATTCATCTTTCTTTTATTTGT--CTGTTTTAGTTAAAAA 112

Oy	271	tgaactagcgcgacgactgatattcgagaatg	301
Db	113	TGAACCTAACCAACGACAATATTCGAGAGAC	143

RESULT 5
US-08-390-878-16/c
; Sequence 16, Application US/08390878
; Patent No. 5700683

:
:
: APPLICANT: Stover, Charles K.
: APPLICANT: Mahlars, Gregory G.
: TITLE OF INVENTION: VIRULENCE-ATTENUATING GENETIC DELETIONS
:
: NUMBER OF SEQUENCES: 18
:
: CORRESPONDENCE ADDRESS: :
:

ADDRESSEE: Townsend and Townsend Kroule and Crew
STREET: One Market Plaza, Steuart Street Tower, 20th
STREET: Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Patent-in Release #1.0, Version #1.30
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/390,878
 ? FILING DATE: 17-FEB-1995
 ? CLASSIFICATION: 435
 ? ATTORNEY/AGENT INFORMATION:
 ?

```

; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 15371A-17
; TELECOMMUNICATION INFORMATION:

```

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; TELEPHONE: 415/543/9600
;
; TELEFAX: 415/543/5043
;
; INFORMATION FOR SEQ ID NO: 16:
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; SEQUENCE CHARACTERISTICS:

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; LENGTH: 16885 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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US-08-390-878-16

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Query Match	10.1%;	Score 32;	DB 1;	Length 16885;
Best Local Similarity	55.4%;	Pred. No. 0.55;		
Matches 62;	Conservative 0;	Mismatches 50;	Indels 0;	Gaps 0;

OY 31 ccttccttgcacatagagtgtgatgvtlgtcgtactagttcccttaaccatatgaagtggcgca 90
||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5391 ccgccgattggcganccgggggtgtgggtgcttttaganccggcccgttccggccaaggccgcc 5332

Qy 91 lctgctggggcccaattgcatacgtcgctbgaaagctctatatattgcccgtcgg 142
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5331 TTTCTTGGCGGCATCGGCAATCGAGTGTGGCGGAGGCGGAGTGCGGCTGGGG 5280

RESULT 6
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A

;
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.

```

: TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
:
: TITLE OF INVENTION: TUBERCULOSIS
:
: FILE REFERENCE: 24366-20007.00
:
: CURRENT APPLICATION NUMBER: US/09/103,840A

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; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
;

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: TYPE: DNA
: ORGANISM: Mycobacterium tuberculosis
: FEATURE:
: OTHER_INFORMATION: CDC_1551
: OTHER_INFORMATION: "n" bases at various positions throughout the sequence
: OTHER_INFORMATION: represent a, t, c or g
: OS-09-103-840A-2

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Query Match	10.1%;	Score 32;	DB 4;	Length 4403765;
Best Local Similarity	55.4%;	Pred. No. 10;		
Matches 62;	Conservative 0;	Mismatches 50;	Indels 0;	Gaps 0;

31 cccctccctgaacatagaggttgatagtggtgtcctcaggtccctcaacacatagacggtggtgcgca 90
Db 4345576 CCGCAGTGGGCGATGGGGGGGCTGTGGGGTGTAGATCCGGCCCGCTCCGGCCAGCGCGGC 4345517

Dy 91 tctgctggggccaattgcatacgtcgctgtaagaactatatttgccgtcgcg 142
||| ||| ||| | |||| | ||| | ||| ||| |||
Db 4345516 TCTCCTCCGGCGATTCGCAATCGAGTTGCACGAGCGCGAGGTGGGGTGGGG 4345465

RESULT 7
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A

; APPLICANT: FLEISCHMAN, Robert D.
 ; APPLICANT: WHITE, Owen R.
 ; APPLICANT: FRASER, Claire M.

FILE OF INVENTION: DNA SEQUENCES FOR CYTILIN HINDIII² IN MICROORGANISMS
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-2007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A

```

; NUMBER OF SEQ ID NOS. 2
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;
; LENGTH: 4411529
;

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; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match	10.1%;	Score 32;	DB 4;	Length 4411529;
Best Local Similarity	55.4%;	Pred. No. 10;		
Matches 62;	Conservative 0;	Mismatches 50;	Indels 0;	Gaps 0;

NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Leydig, Voit & Mayer, Ltd.
 STREET: Two Prudential Plaza, Suite 4900
 CITY: Chicago
 STATE: IL
 COUNTRY: US
 ZIP: 60601-6780
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/581,148C
 FILING DATE: 29-DEC-1995
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Larcher, Carol
 REGISTRATION NUMBER: 35243
 REFERENCE/DOCKET NUMBER: 71380
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 616-5600
 TELEFAX: (312) 616-5700
 INFORMATION FOR SEQ ID NO: 30:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6343 bases
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: Zea mays
 INDIVIDUAL ISOLATE: 2.mays Glossy2 locus DNA
 US-08-581-148C-30

Query Match 9.2%; Score 29.2; DB 3; Length 6343;
 Best Local Similarity 74.0%; Pred. No. 3.2;
 Matches 37; Conservative 0; Mismatches 13; Indels 0; Gaps 0.

Db 3878 ACGTACCTCCCTCGTCCTTTTATTATTCGTTCTTGGTCACAGATCA 3927
 Gc 224 aagctctccctcgtttttttattatcgctcggtttgttaacatga 273
 ||||||| ||||| ||||| ||| || ||||| |||

RESULT 11
 US-08-030-096-3
 Sequence 3, Application US/08030096
 Patent No. 5426041
 GENERAL INFORMATION:
 APPLICANT: Fabijanski, Steven F.
 TITLE OF INVENTION: BINARY CRYPTOXYTOXIC METHOD OF HYBRID
 TITLE OF INVENTION: SEED PRODUCTION
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington, D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/030,096
 FILING DATE: 22-MAR-1993
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/556,917

```

      FILING DATE: 20-JUL-1990
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: PCT/CA91/00255
        FILING DATE: 22-JUL-1991
      ATTORNEY/AGENT INFORMATION:
        NAME: BENT, Stephen A.
        REGISTRATION NUMBER: 29,768
        REFERENCE/DOCKET NUMBER: 33229/164/PIHI
      TELECOMMUNICATION INFORMATION:
        TELEPHONE: (202)672-5300
        TELEFAX: (202)672-5399
        TELEX: 904136
      INFORMATION FOR SEQ ID NO: 3:
        SEQUENCE CHARACTERISTICS:
          LENGTH: 8585 base pairs
          TYPE: nucleic acid
          STRANDEDNESS: double
          TOPOLOGY: linear
        MOLECULE TYPE: DNA (genomic)
      FEATURE:
        NAME/KEY: CDS
        LOCATION: join(308..370, 1136..1261, 6369..6428, 7198..7353)
US-08-030-096-3

Query Match           9.1%, Score 28.8; DB I: Length 8585;
Best Local Similarity 52.5%; Pred.No. 5.3;
Matches 63; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Oy   154 atcatactgtgctgaggaagaagcgctgcaggccttcgaaacaaaactgatlttgcygt 213
      |||||
Db   6983 ACCATATTTTTCACAAAATAAAATAAAGTGTGACCAACCATVTCGCATTTTTTTTT 7042

Oy   214 ttctgctgaagtactccctccgcttttattatcgtcgcgttatgaaccaatga 273
      ||||| || || ||||| || | ||||| || ||||| || ||||| ||
Db   7043 ATATCTGCGCAAATATATTCTTTTCTTTTACTTATTAAGCTTTAAATGAATGTTA 7102

RESULT 12
US-07-960-389-1/c
Sequence 1, Application US/07960389
Patent No. 5705611
GENERAL INFORMATION:
APPLICANT: HAYASHIDA, Kasuhiko;
TITLE OF INVENTION: Human GM-CSF Receptor Component
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disc
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System Software 7.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/960,389
FILING DATE: 07-JAN-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 554,745
FILING DATE: 18-JUL-1990
APPLICATION NUMBER: PCT/US 91/04846
FILING DATE: 16-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Blasdale, John H. C.
REGISTRATION NUMBER: 31,895
REFERENCE/DOCKET NUMBER: DX01430
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 298-2902

```

TELEFAX: (908) 298-5388
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3475 base pairs
TYPE: nucleotides
STRANDEDNESS: single
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: human
FEATURE:
OTHER INFORMATION: DNA sequence encoding Human GM-CSF receptor
US-07-960-389-1

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Best Local Similarity 49.7%; Pred. No. 5.3;
Matches 72; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
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DB 1254 CTCACATCCTTGTCACGTTGAGGATGGAGGGCCATCTGATGTTCACTGAGCTCTTTA 1195
QY 128 ttttggcgctcgagcaggaacacatatactgctgaggaagcgctgagggct 187
DB 1194 TGTGTTTCTCTGCCCTCTTGCGCTGACAGACATGATTTGGCCGTGGGTGGGGGT 1135
QY 188 ctcaagacaaaactgatttggtg 212
DB 1134 CGGCGACGGGAACTGTGCGAGTGTG 1110

RESULT 13
US-08-714-918-76/c
Sequence 76, Application US/08714918
Patent No. 6037123
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Ying J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,918
FILING DATE: September 13, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 222/005
TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 3305 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-714-918-76

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QY 240 ttttctatcgctggttttagtcaacatgaactagcgagcactgatatcgagaa 299
DB 729 CATTTGTTTCAAGCGCTAATCTTTGAAAAATTTACTAGCTACATATTAATTGCAAAAT 670
QY 300 tgaaggg 306
DB 669 TAAACGG 663

RESULT 14
US-09-265-315-76/c
Sequence 76, Application US/09265315
Patent No. 6187541
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Ying J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 3, 2002, 05:09:52 ; Search time 5254.53 seconds
(without alignments)
1545.237 Million cell updates/sec

Title: US-09-300-482-298

Perfect score: 388

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
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10: gb_ro:*
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12: gb_sy:*
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18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
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26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
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2	226.6	58.5	922	8	AF370479	AF370479	Arabidops
3	122.6	31.6	12091	1	AE006493	AE006493	Streptoco
4	112.8	29.1	10029	1	AE006423	AE006423	Lactococc
5	96.8	24.9	1316	10	BC019126	BC019126	Mus muscu
6	96.8	24.9	2357	10	BC006953	BC006953	Mus muscu
7	95.2	24.5	338579	1	AP003004	AP003004	Mesorhizo
8	91.4	23.6	313450	1	AL596170	AL596170	Listeria
9	90.2	23.2	347050	1	AL591981	AL591981	Listeria
10	88.8	22.9	1205	6	AX085734	AX085734	Sequence
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12	88.8	22.9	2501	9	BC005148	BC005148	Homo sapi
13	88.8	22.9	3556	6	AR129150	AR129150	Sequence
14	88	22.7	10029	1	AE009551	AE009551	Brucella
15	87.2	22.5	303249	1	AP001515	AP001515	Bacillus
16	85.2	22.0	927	33	AC057311	AC057311	Giardia
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18	80.8	20.8	11208	1	AE008544	AE008544	Streptoco
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22	79.2	20.4	137952	2	SPNEU1909	SPNEU1909	Streptoco
23	79.2	20.4	163443	2	AC006280	AC006280	Plasmodiu
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25	79	20.4	911	8	SCPE0518	SCPE0518	S.cerevisia
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27	78.6	20.3	5960	1	RCU23145	RCU23145	Rhodobacter
28	78.2	20.2	921	3	AY061110	AY061110	Drosophill
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32	77.4	19.9	131278	2	AC108753	AC108753	Oryza sat
33	76.4	19.7	10150	1	AE002217	AE002217	Chlamydia
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36	76	19.6	306250	1	SM591788	SM591788	Sinorhizo
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38	75.4	19.4	993	12	AF070942	AF070942	Expressio
39	75.4	19.4	1198	8	SPR5P3E	SPR5P3E	Splinaclia
40	75.4	19.4	1230	8	AF070941	AF070941	Splinaclia
41	75	19.3	67712	8	AC022355	AC022355	Arabidops
42	74.2	19.1	3400	1	TP097573	TP097573	Treponema
43	74.2	19.1	10081	1	AE001263	AE001263	Treponema
44	74.2	19.1	39729	8	SPAC31G5	SPAC31G5	S.pombe chr
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ALIGNMENTS

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LOCUS	AF189365
DEFINITION	Oryza sativa D-ribulose-5-phosphate 3-epimerase mRNA, complete cds.
ACCESSION	AF189365
VERSION	AF189365.1 GI:6007802
KEYWORDS	
SOURCE	Oryza sativa.
ORGANISM	Oryza sativa Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE	1 (bases 1 to 930)
AUTHORS	Kopriva,S., Koprivova,A. and Suss,K.H.
TITLE	Identification, cloning, and properties of cytosolic
REFERENCE	D-ribulose-5-phosphate 3-epimerase from higher plants
JOURNAL	J. Biol. Chem. 275 (2), 1294-1299 (2000)
MEDLINE	2 (bases 1 to 930)
AUTHORS	Kopriva,S., Koprivova,A. and Suss,K.-H.
TITLE	Direct Submision
JOURNAL	Submitted (20-SEP-1999) Institute of Forest Biology and Tree
	Physiology, Am Flughafen 17, Freilburg Im Breisgau 79085, Germany

FEATURES	source	Location/Qualifiers
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Matches	286; Conservative 0; Mismatches 77; Indels 0; Gaps 0;	
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OY	146 tgtccccaattaaactatlttgcgctccagattatgaaagtttgagaagaacacacaaggc 205	
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OY	206 atattgattgtcaccttatgtgttaacaatcccttgaattatgttgaaccttggosaa 265	
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OY	266 agcttgctcttcgtgtttacatcttcacgttagagacacacaaagaataacttgaanaagact 325	
Db	289 AGCTGTGCTCCAGGTTTCACATCTCCATATGAAAGTAATCCAGAGACATTTGGCAAGACT 348	
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Db	409 TGT 411	
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DEFINITION	Arabidopsis thaliana putative D-ribulose-5-phosphate 3-epimerase (F28J1.18)	mRNA, complete cds.
ACCESSION	AF370479	
VERSION	AF370479.1	GI:13877556
KEYWORDS	FLI_CDNA.	
SOURCE	thale cress.	
ORGANISM	Arabidopsis thaliana	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	
REFERENCE	1 (bases 1 to 922)	
AUTHORS	Lam, B., Southwick, A., Karlin-Neumann, G., Nguyen, M., Miranda, M., Palm, C.-J., Bowers, L., Jones, T., Banb, J., Carmlin, P., Chen, H., Cheuk, R., Chung, M. K., Hayashizaki, Y., Ishida, J., Kamiya, A., Kawai, C., Kim, C., Lin, J., Liu, S. X., Narusaka, M., Pham, P. K., Sakano, H., Sakurai, T., Satou, M., Seki, M., Shino, P., Yamada, K., Shinozaki, K., Ecker, J., Theologis, A. and Davis, R. W.	

TITLE Direct Submission
JOURNAL Submitted (17-APR-2001) DNA Sequencing and Technology Center,
Stanford University, 835 California Avenue, Palo Alto, CA 94304,
USA
COMMENT e-mail for correspondence: arab@sequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFI cDNAs (RAFI cDNA : 'RIKEN Arabidopsis Full-Length cDNA') : Seki,M., Narusaka,M., Ishida,J., Saitou,M., Kamuya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

The Saik, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFI cDNAs: Lam,B., Karlin-Newmann,G., Nguyen,M., Southwick,A., Miranda,M., Palm,C.J., Bowser,L., Jones,I., Banh,J., Chen,H., Cheuk,R., Chung,M.K., Kim,C., Lin,J., Liu,S.K., Pham,P.K., Sakano,H., Shim,P., Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.

Lam,B., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as PIs.

FEATURES
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BASE COUNT 230 a 212 c 237 g 243 t

ORIGIN

Query Match 58.5%; Score 226.8; DB 8; Length 922;
Best Local Similarity 75.4%; Pred. No. 1.5e-52;
Matches 282; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

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Db AAGAAGATGATGTGCCCAATAATACACCGTCGATGCTGCATCGGACTTGCCAATCTA 104

OY 75 gcttccagaggtcagcgatgtctccacttggtggcgcgagtgtgctcccaaatgacatca 134
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OY 135 gatggacatttgcgccaaacttaactatctggcgctcacgatttatgaaagttagaaga 194
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Db GACGGGCATTTTGTCGCCAATCTTAACGATTGTGTGCTCTCTGTCATCGAGAGTTTGGCAGAG 224

OY 195 cacacaagaagcatatttgatttgtacccttaagtgtttacaatatccctctgattattgttaa 254
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Db CACACTAATGATATCTTGATGTGCACCTTATGTGTGAGAACCCCATGATGATTAGTTCA 284

OY 255 cccttgcgaanaagctgtggtcttggttttcatttcaacgaaagacatacaagaataaac 314
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Db CAGATGCTTAAGCTGGGGCTTGTGGTTTCACATTTCCACGTCGAGGTGGCCCCAAGATAT 344

OY 315 ttgaaaagaacttaccaagaatacaagtccaatgacatgacatgattctctgtgtagcatctaa 374
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Db 345 TGGCAACAACCTTCTCGAGAGATTAACTACTGAGTACAGACCGCTGCGCTTAAG 404
Oy 375 cctcggagaccocct 388
11111 11111 11111
Db 405 CCGGAACACCTCT 418

RESULT 3
AE006493
LOCUS
DEFINITION Streptococcus pyogenes M1 GAS strain SF370, section 22 of 167 of the complete genome.
ACCESSION AE006493 AE004092
VERSION AE006493.1 GI:13621538
KEYWORDS
SOURCE Streptococcus pyogenes M1 GAS.
ORGANISM Streptococcus pyogenes M1 GAS.
Bacteria: Firmicutes; Bacillus/Clostridium group; Streptococcaceae; Streptococcus.
1 (bases 1 to 12091)
REFERENCE
AUTHORS Ferretti,J.J., McShan,W.M., Adjic,D., Savic,D., Savic,G., Lyon,K., Primeaux,C., Sezate,S.S., Surorov,A.N., Kenton,S., Lal,H., Lin,S., Qian,Y., Jia,H.G., Najjar,F.Z., Ren,Q., Zhu,H., Song,L., White,J., Yuan,X., Clifton,S.W., Roe,B.A. and McLaughlin,R.E.
Direct Submission
TITLE Submitted (10-APR-2001) Department of Microbiology and Immunology, University of Oklahoma Health Sciences Center, 940 St Young Blvd, Oklahoma City, OK 73104 USA
JOURNAL
PUBMED
REFERENCE
AUTHORS
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CDS

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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 1316)
 Strausberg, R.
 Direct Submission
 Submitted (07-DEC-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK
 COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@nih.gov

Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
 Benjamini, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaapi, R.,
 Lim, M., Maduro, Q.L., Mastaglio, C., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J.,
 Tjongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
 Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
 Series: IRAC Plate: 39 Row: e Column: 7
 This clone was selected for full length sequencing because it
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 Location/Qualifiers
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BASE COUNT 392 a 253 c 314 g 357 t
 ORIGIN

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 Db 133 ATGCTGAGACTGGGGCGCGCTACCTGCACCTGATGATGACGCGCATTTTGTCC 192
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 VERSION BC006953.1 GI:13905310
 KEYWORDS MGC.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 2357)
 Strausberg, R.
 Direct Submission
 Submitted (27-APR-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK
 COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Lotmar Hennighausen Ph.D., Robin Humphreys
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

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CDS
CDS

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CDS

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ACCESSION	AL596170 AL592022		
VERSION	AL596170.1 GI:16414292		
KEYWORDS	.		
SOURCE	Listeria innocua.		
ORGANISM	Listeria innocua Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Listeria. 1 (sites)		
REFERENCE	Glaser,P., Frangeul,L., Buchrieser,C., Rusniok,C., Amend,A., Baquero,F., Berche,P., Bloeker,H., Brandt,P., Chakraborty,T., Charbit,A., Chehouani,F., Couve,E., de Daruvar,A., Dehoux,P., Domann,E., Dominguez-Bernal,G., Duchaud,E., Durant,L., Dussurget,O., Etikian,K.D., Fshih,H., Portillo,F.G., Garrido,P., Gaetler,L., Goebel,M., Gomez-Jopez,N., Hain,T., Hauf,J., Jackson,D., Jones,L.M., Kaerst,U., Kreft,J., Kuhn,M., Kunst,F., Kutaprat,G., Madueno,E., Maitouram,A., Vicente,J.M., Ng,E., Neujahr,H., Nordisiek,G., Novella,S., de Pablo,B., Perez-Diaz,J.C., Purcell,R., Remmel,B., Rose,M., Schueter,T., Simoes,N., Tierrez,A., Vazquez-Boland,J.A., Voss,H., Weiland,J. and Cossart,P. Comparative genomics of Listeria species Science 294 (5543), 849-852 (2001) 2 (bases 1 to 313450) 21537279		
TITLE	Glaser,P., Frangeul,L. and Rusniok,C.		
JOURNAL	Submitted (09-JUL-2001) Glaser P., Institut Pasteur, Genomique des Microorganismes Pathogenes, 25 rue du Docteur Roux, 75724 Paris Cedex 15, FRANCE E-mail: pglaser@pasteur.fr Phone: +33 (0)1 45 68 89 96, Fax: +33 (0)1 45 68 87 86.		
COMMENT	Location/Qualifiers		
FEATURES	source		
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tRNA			

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SOURCE Listeria monocytogenes.
ORGANISM Listeria monocytogenes.
REFERENCE 1 (sites)
AUTHORS Glasner,P., Frangeul,L., Buchrieser,C., Rusnok,C., Amend,A.,
Baquero,F., Berche,P., Biocker,H., Brandt,P., Chakraborty,T.,
Charbit,A., Chetoui,M., Couve,E., de Daruvar,A., Delnoux,P.,
Domann,E., Dominguez-Bernal,G., Duchaud,E., Durant,L.,
Dussurget,O., Entian,K.D., Fsiil,H., Portillo,F.G., Garrido,P.,
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Kurapkai,G., Maduno,E., Maitournam,A., Vicente,J.M., Ng,E.,
Nedjari,H., Nordstedt,G., Novella,S., de Pablo,B., Perez-Diaz,J.C.,
Purcell,R., Rammel,B., Rose,M., Schlueter,T., Simoes,N.,
Tierrez,A., Vazquez-Boland,J.A., Voss,H., Wehland,J. and Cossart,P.
Comparative genomics of Listeria species
Science 294 (5543), 849-852 (2001)
TITLE JOURNAL MEDLINE 2 (bases 1 to 347050)
REFERENCE 21537279
AUTHORS Glasner,P., Frangeul,L. and Rusnok,C.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-2001) Glasner P., Institut Pasteur, Genomique des
Microorganismes Pathogenes, 25 rue du Docteur Roux, 75724 Paris
Cedex 15, FRANCE
COMMENT E-mail: p.glasner@pasteur.fr
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VERSION
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SOURCE Bacillus halodurans DNA.
ORGANISM Bacillus halodurans
Bacteria; Firmicutes; Bacillus/Clostridium group;
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REFERENCE AUTHORS TITLE	Bacillus/Staphylococcus group; Bacillus. 1 (sites) Takami,H. and Horikoshi,K. Reidentification of facultatively alkaliphilic Bacillus sp. C-125 to Bacillus halodurans
JOURNAL REFERENCE AUTHORS	Biosci. Biotechnol. Biochem. 63, 943-945 (1999)
TITLE	2 (sites) Takami,H., Takaki,Y., Nakasone,K., Sakiyama,T., Maeno,G., Sasaki,R., Hiramata,C., Fujii,F. and Masui,N. Genetic analysis of the chromosome of alkaliphilic Bacillus halodurans C-125
JOURNAL MEDLINE REFERENCE AUTHORS	Extremophiles 3 (3), 227-233 (1999) 99411980
TITLE	3 (sites) Takami,H., Nakasone,K., Hiramata,C., Takaki,Y., Masui,N., Fujii,F., Nakamura,Y. and Inoue,A. An improved physical and genetic map of the genome of alkaliphilic Bacillus sp. C-125
JOURNAL MEDLINE REFERENCE AUTHORS	Extremophiles 3 (1), 21-28 (1999) 99104645
TITLE	4 (sites) Takami,H., Masui,N., Nakasone,K. and Horikoshi,K. Replication origin region of the chromosome of alkaliphilic Bacillus halodurans C-125
JOURNAL MEDLINE REFERENCE AUTHORS	Biosci. Biotechnol. Biochem. 63 (6), 1134-1137 (1999) 9936711
TITLE	5 (sites) Takami,H., Takaki,Y., Nakasone,K., Hiramata,C., Inoue,A. and Horikoshi,K. Sequence analysis of a 32-kb region including the major ribosomal protein gene clusters from alkaliphilic Bacillus sp. strain C-125
JOURNAL MEDLINE REFERENCE AUTHORS	Biosci. Biotechnol. Biochem. 63 (2), 452-455 (1999) 99290908
TITLE	6 (sites) Takami,H. Genome analysis of facultatively alkaliphilic Bacillus halodurans C-125
JOURNAL REFERENCE AUTHORS	Extremophiles in deep-sea environments, 249-284 (1999) 7 (sites) Takami,H., Nakasone,K., Ogasawara,N., Hiramata,C., Nakamura,Y., Masui,N., Fujii,F., Takaki,Y., Inoue,A. and Horikoshi,K. Sequencing of three lambda clones from the genome of alkaliphilic Bacillus sp. strain C-125
JOURNAL MEDLINE REFERENCE AUTHORS	Extremophiles 3 (1), 29-34 (1999) 99184646
TITLE	8 (sites) Takami,H. and Horikoshi,K. Analysis of the genome of an alkaliphilic Bacillus strain from an Industrial point of view
JOURNAL MEDLINE REFERENCE AUTHORS	Extremophiles 4 (2), 99-108 (2000) 20263314
TITLE	9 (sites) Nakasone,K., Masui,N., Takaki,Y., Sasaki,R., Maeno,G., Sakiyama,T., Hiramata,C., Fujii,F. and Takami,H. Characterization and comparative study of the rrr operons of alkaliphilic Bacillus halodurans C-125
JOURNAL MEDLINE REFERENCE AUTHORS	Extremophiles 4 (4), 209-214 (2000) 20426005
TITLE	10 (sites) Takami,H., Nakasone,K., Takaki,Y., Maeno,G., Sasaki,R., Masui,N., Fujii,F., Hiramata,C., Nakamura,Y., Ogasawara,N., Kuhara,S. and Horikoshi,K. Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis
JOURNAL MEDLINE REFERENCE AUTHORS	Nucleic Acids Res. 28 (21), 4317-4331 (2000) 20512582
TITLE	11 (bases 1 to 303249) Takami,H. and Takami,Y. Direct Submission Submitted (22-MAR-2000) Hideto Takami, Japan Marine Science and Technology Center, Deep-sea Microorganisms Research Group, 2-15 Natsushima, Yokosuka, Kanagawa 237-0061, Japan (E-mail:takami@jamstec.go.jp,

COMMENT FEATURES source	URI: http://www.jamstec.go.jp/jamstec-e/bio/DEEPSTAR/Research.html , Tel:81-468-67-3895, Fax:81-468-66-6364) On Jan 31, 2001 this sequence version replaced gi:10174886. Location/Qualifiers 1. 303249 /organism="Bacillus halodurans" /db_xref="taxon:86655" /note="alkaliphile" 104. .1102 /gene="BH2267" 104. .1102 /gene="BH2267" /codon_start=1 /transl_table=1 /product="penicillin-binding protein" /protein_id="BAB05986.1" /db_xref="GI:10174887" /translation="MKNHHTIMEDKLSGTALMKKGGEDIPFTASGFANRKRIPNE HHTREGIASGCKLPTAATCOLYEACKLSSTDPPLSLMDLAPPPNVTIHLTLHTSGVP DYRDEETIDPDEFIDKMDVPTILRLRDLPLRQHPA PKRPPGRHRYNNAGFLLGL VSSVSGVTRQEVYEVANVQRAGMHSYGFAEDTLPAKALGIDLEDSMTNLYSL PVIGSDSGAVYVAEDMMKLMALMHSEILNETYTGKLTLPVHCEDDDYGYGVAIK QDGAISKYHVMGYDPVCFHSAFYPTSNIGYVVCANQSSGAVDVAALAEALFSEA" complement(1146. .1469) /gene="BH2268" complement(1146. .1469) /gene="BH2268" /note="BH2268 unknown" /codon_start=1 /transl_table=1 /protein_id="BAB05987.1" /db_xref="GI:10174888" /translation="MKVITLDSGTFKRFKPEQASAYLLKLGHVLSVGFEEQSEIEI TEQVQVFENHRRKTEMSDELIVLDVDEYIGRSTRKEITFAFSKGMIRYSESELA STYFS" complement(1636. .2373) /gene="BH2269" complement(1636. .2373) /gene="BH2269" /note="BH2269 unknown" /codon_start=1 /transl_table=1 /protein_id="BAB05988.1" /db_xref="GI:10174889" /translation="MKKYGILVGFALSTGLMCGOEQEBVEKNIDGASGETPST EETIDINLPPDVATVNGESIDKETYVWLEQMMTMAOYGISLEGESKQMSIIEE OTTEOLINEQLLOQAATEKEIESEEDLEAFVAQFSSEALMEALLEGSSMDE LKEIEHYRQQRKYVEEETEAINTVEETIOAREBEKQYTEDELPTPEELQNSINEOR LIAERQEQLEVLFEKLRDEGDITVHI" complement(2582. .3367) /gene="BH2270" complement(2582. .3367) /gene="BH2270" /codon_start=1 /transl_table=1 /product="ABC transporter (ATP-binding protein)" /protein_id="BAB05989.1" /db_xref="GI:10174890" /translation="MADILQVEQYTLRRKAPRIIQISMOVQGEHMAIYGLNGSKT SLKRTITTEWPTBEGHVAVIGNRGHPVIOVRRIQVMSVMSLDDRHPTKQDPTVEI VLSGHGVGVYEPVIGENDVAKRAALETFTLTLPTPERFLTSSGGRKAFARAVY AKPEFLIDEPPTGIDLARQLQLTESVATVTGAPFLVTHYPELIDPPLTHVLM LKDGHVIAQGRKDEVLKEMTAAFGCSLDVIAQSGRYWAKPM" complement(3378. .4310) /gene="BH2271" complement(3378. .4310) /gene="BH2271" /codon_start=1 /transl_table=1 /product="dipeptidase" /protein_id="BAB05990.1"
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GenCore version 4.5
Copyright (c) 1993 - 2000 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 3, 2002, 03:38:53 ; Search time 6582.52 Seconds
(without alignments)
795.564 Million cell updates/sec

Title: US-09-300-482-298

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Searched: 13736207 segs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
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Listing first 45 summaries

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15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	370	95.4	518	10	BF598003 sv02h10.y
2	365.4	94.2	458	9	AI437973 sa34c12.y
3	352.8	90.9	575	10	BM309659 sak65b08.
4	338.2	87.2	374	10	BM316079 sab55g09.
5	320.8	82.7	403	9	AV412302 AV412302
6	310.4	80.0	405	9	AI442690 AI442690
7	307.8	79.3	574	10	BI308956 BI308956
8	307.8	79.3	641	9	AM682881 AM682881
9	307.8	79.3	654	10	BM455207 BM455207
10	307.8	79.3	683	10	BF645593 BF645593
11	296.8	76.5	597	10	BM451182 BM451182
12	296.8	76.5	613	10	BE325053 BE325053
13	293.2	75.6	666	10	BF634692 BF634692
14	285.4	73.6	736	9	AM348508 AM348508
15	281.2	72.5	399	9	AV425192 AV425192
16	281.2	72.5	448	9	AL371120 AL371120
17	269.8	69.5	467	10	BI124136 BI124136

18	260	67.0	745	10	BM526117
19	250.4	64.5	506	9	AJ412644
20	247	63.7	571	10	BM307768
21	244.6	63.0	613	10	BF261410
22	244.6	63.0	816	9	AM983286
23	244.6	63.0	837	10	BM254937
24	244.6	63.0	838	10	BI951621
25	243.8	62.8	659	10	BM608149
26	243	62.6	488	10	BM606577
27	243	62.6	494	10	BE404347
28	242	62.4	506	10	BM601743
29	241.4	62.2	268	10	BI93749
30	239.8	61.8	417	9	AU165324
31	238.2	61.4	526	10	BE94864
32	237.4	61.2	407	9	AU069503
33	236.6	61.0	454	10	BM483212
34	234	60.3	611	10	BM112847
35	232.4	59.9	669	10	BM599823
36	232.4	59.9	679	10	BM599735
37	232.4	59.9	699	10	BI432299
38	228.8	59.0	694	9	AU164966
39	226.8	58.5	483	9	AV554048
40	226	58.2	497	9	AI490023
41	226	58.2	552	9	AI772355
42	226	58.2	593	9	AM031337
43	226	58.2	630	9	AM223738
44	226	58.2	653	9	AI896020
45	226	58.2	729	10	BI928671

ALIGNMENTS

RESULT 1
LOCUS BF598003 558 bp mRNA linear EST 06-DEC-2001
DEFINITION sv02h10.y1 Gm-cl056 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl056-764 5' similar to TR:Q9SE42 Q9SE42 D-RIBULOSE-5-PHOSPHATE 3-EPIMERASE ; , mRNA sequence.

ACCESSION BF598003
VERSION BF598003.1 GI:11690327

KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max

REFERENCE 1 (bases 1 to 558)
AUTHORS Shoemaker,R., Kelm,P., Vodkin,L., Erpelting,J., Corryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Rheising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

FEATURES
source
1..558
/organism="Glycine max"
/db_xref="taxon:3847"

High quality sequence stop: 412.
Insert Length: 951 Std Error: 0.00
Location/Qualifiers

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/clone="GENOME SYSTEMS CLONE ID: Gm-cl056-764"
/clone.lib="Gm-cl056"
/tissue.type="Whole seedling, 4 day old"
/lab.host="DH10B"
/notes="vector: plusscript II SK+; Site_1: EcoRI; Site_2:
XhoI. The cDNA library was constructed from mRNA isolated
from 4 day old seedling of P1468916. The seedlings were
germinated in a growth chamber using germination paper.
Complementary DNA was synthesized from mRNA using a primer
consisting of a poly(dT) sequence with a XhoI restriction
site. EcoRI adapters were ligated to the blunt-ended cDNA
fragments followed by XhoI digestion. The cDNA fragments
were directionally cloned into the EcoRI-XhoI restriction
site of the plusscript vector. The ligated cDNA fragments
were transformed into DH10 host cells (GibcoBRL). This
library was constructed in the laboratory of Dr. Randy
Shomatter."

```

Query Match	95.4%;	Score 370;	DB 10;	Length 558;
Best Local Similarity	97.4%;	Pred. No. 4e-96;		
Matches 376;	Conservative	0;	Mismatches 10;	Indels 0;
			Gaps	0;

OY	3	agbaaagaagaaagatggygaatgacacggaaatagtcttccttgaigtctcttcgcac	62
Db	49	AGAAAAAGAAAGGAGATGGAGTGCACACCGAAATGCTCTTCGATGCTCTTCGAC	108
OY	63	ttcgcgaatttggtcttcgcgaagctcaaggcatgctccactttgggocgatttggtccac	122
Db	109	TTGCGCAATTGGCTTCGACAGCTCAAGCGCATGCTCCACTTTGGGGCCATTGGGCTCCAC	168
OY	123	atggacatcaatgatatgggcatcttgctcccaattaaactatgagctcgcagttatgaa	182
Db	169	ATGGACATCATGATGGATGGGCACTTTGTCCCAATTAACTATGGGGCTCCACTTATTGAA	228
OY	183	agtttgagaagacacacaaagycataattgatatctcaactatgatttacaatccctt	242
Db	229	AGTTTGAGAAACACACAAAGGCAATTTGGATGTCACTTAATGTTAAACAATCCTCTT	288
OY	243	gattatgtctgaaccccttgacaaagctbgtgctcttggttttaacttcaactgaagagaca	302
Db	289	GATTATGTGTGAACCTTGTGGCANAAACCTGTGCTTGTGTTTACATTTCAATGAGAGACA	348
OY	303	tcaaaagaatcaacttggaaaagactltccaaagaatcgaagtcacatgagatgatctcgt	362
Db	349	TCAAAAGATTAATCGGAGAGAACTTATCCAAAGAATCAAGTCACATGATCATCTCTAGT	408
OY	363	gtagatattaagccctgggaaccccgct	388
Db	409	GTAGCATTTAAAGCCCTGGAGCCCCCAT	434

RESULT	2
AI437973	
LOCUS	418 bp mRNA linear EST 28-NOV-2001
DEFINITION	sa3c1002.y1 Gm-cl004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: sa3c1004-1199 5' similar to: TR:014105 014105 RIBULOSE-PHOSPHATE 3-EPIMERASE. ; mRNA sequence.
ACCESSION	

ACCESSION	AI437973
VERSION	AI437973.1
KEYWORDS	GI:4289768
SOURCE	EST.
	soybean.

ORGANISM
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseolaceae
Glycine.

REFERENCE 1 (bases 1 to 418)

AUTHORS

Snowman, K., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers

TITLE	JOURNAL	COMMENT
Public Soybean EST Project	Unpublished (1999)	Contact: Shoemaker R/Public Soybean EST project

Y. Person, B. Swaller, T. Gibbons, M. Pape, D. Harrey, N. Schurr
R. Ritter, E. Kohn, S. Shm, T. Jackson, Y. Cardens, M., McConn
R. Waterson, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Reagen, Invitrogen Corp., 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: cust@reagen.com
Insert Length: 945 Std Error: 0.00
Seq primer: -40RP from Gibco
High quality sequence stop: 414
POLYA-No.

FEATURES	Location/Qualifiers
Source	110

Source

	BASE COUNT	
111	a	113 t
93 c	101 g	

/organism="Glycine max"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl004-1199"
 /clone_1lb="Gm-cl004"
 /clone_type="root"
 /lab_host="XL10-Gold"
 /note="vector: pBluescript II Xr; Site_1: EcoRI; Site_2: XhoI; root cDNA. The mRNA was isolated from entire roots of 8 day old 'Williams' seedlings which were propagated on paper towels with distilled water. Stratagene's cDNA Synthesis kit (catalog #200401) was used to synthesize the cDNA. First- strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA is hemethylated. Stratagene's first-strand synthesis primer was used (GAGACAGACAGACAGACAGACAGACCTAGCTCAGCTT-18). After second-strand synthesis, the cDNA ends were 'polished' with clone pfu DNA polymerase, ligated to EcoRI adapters, and phosphorylated. The XhoI site within the first-strand synthesis primer was restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GIBCOBRL Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript II Xr predigested vector (pBluescript II SK(+)) that had been digested with EcoRI and XhoI, and phosphorylated). Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts. Blue colonies 9n-15) have been sequenced, and possess putative cDNA inserts. This library was constructed by Dr. Paul Keim & Virginia H. Coryell, Department of Biology, Box5640, Northern Arizona University, Flagstaff, AZ 86011, Phone: 520-523-1078 (Dr. Paul Keim), 520-523-1372 (Virginia H. Coryell), Fax: 520-523-7500, email: paul.keim@nau.edu, virginia.coryell@nau.edu

Query Match	94.2%	Score 365.4;	DB 9;	Length 418;
Best Local Similarity	97.1%;	Pred. No. 7.8e-95;		
Matches 372;	Conservative	0;	Mismatches 11;	Indels 0;

Qy 6 aagaagaagaatggygaatgacacgaanaatgcttcctgcagctcctcgcagcttc 65
 1 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 4 AGGAAGGAAGGTGGACTGACACCGAAATGCTCCTCGATGCTCTCCGACTTC 63

66 gccaatlttgcttcgaggtcagcgcatgtctccacttcggcgccgatttgctccacatg 125

[illegible]

126 gacatcatgtagtgcattttgtcccaatttaactatattgacgcctccagattattgaaact 185

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|||||
Db 124 GACATCATGATGAGCGCATTTTGTCCCAATTATTTACTATTGCGCTCCAGTATTGAAAGT 183
Oy 186 ttgaagaagacacaaaggacatatttgatgtgcacctatggttacaatcctctgat 245
Db 184 TTGAGAAGACACAAAGGATATTGATGATTCACCTATGTTGCAAAATCCTCTTGAT 243
Oy 246 tatgttgaaaccttggtcaaaagctgtgtcttcgtgtttacattcaatcgtagaacatca 305
Db 244 TATGTTGAGCCCTTGCCAAAGCTGTGCTTTCGTTTACATTTCATGTAGAGACATCA 303
Oy 306 aaagataactggaagaactatccaaagaatcaatgacatgacatgattcctggtga 365
Db 304 AAAGATTAAGTGGAGACACTTATTCACAAAGATCAAGTACATGACATGACTCTGTTGTA 363
Oy 366 gcaatlaagccttggaaccccgct 388
Db 364 GCATTAAAGCTGTGAGACCCCAT 386

RESULT 3
BM309659 575 bp mRNA linear EST 02-JAN-2002
LOCUS sak65b08.y1 Gm-cl036 Glycine max cDNA clone SOYBEAN CLONE ID:
DEFINITION Gm-cl036-7767 5' similar to TR:Q9SE42 Q9SE42 D-RIBULOSE-3-PHOSPHATE
3-EPIMERASE ; mRNA sequence.
ACCESSION BM309659
VERSION BM309659.1 GI:18041365
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 575)
Shoemaker,R., Kelm,P., Vodkin,L., Erpelting,J., Corryell,V., Khanna
,A., Bolla,B., Matra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available through: Resgen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccuteresgen.com web site:
www.resgen.com
Seq primer: -40RP from gibco
High quality sequence stop: 418.
Location/Qualifiers
1. 575
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-cl036-7767"
/clone_1ib="Gm-cl036"
/lisuse_type="somatic embryos cultured on MSD 20"
/lab_host="DH10B"
/note="Vector: pSPORT1. Site_1: NotI. Site_2: SalI. This
cDNA library was constructed from mRNA isolated from
somatic embryos (age ranging from 2 months to 9 months)
cultured on MSD 20. The library was prepared using the
Life Technologies pSuperScript cDNA library construction
kit. Complementary DNA was synthesized from mRNA using a
poly (dT) sequence with a NotI restrictions site. SalI
linkers adapters were ligated to the blunt-ended cDNA

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fragments followed by NotI digestion. The cDNA fragments
were directionally cloned into the NotI-SalI restriction
site of the pSPORT1 vector. The ligated cDNA fragments
were transformed into E.coli Electromax DH10B host cells.
This library was constructed in the laboratory of Dr. Lila
Vodkin by Anu Khanna at the University of Illinois at
Urbana-Champaign. e-mail: l-vodkin@uiuc.edu"
BASE COUNT 156 a 119 c 142 g 157 t 1 others
ORIGIN

Query Match 90.9%; Score 352.8; DB 10; Length 575;
Best Local Similarity 98.1%; Pred. No. 3.8e-91;
Matches 357; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 25 tgacaccgaaatagctccttcgatgctctcttcgacctcgcgaatttgcttcgagg 84
Db 1 TGACACCGAAATTTGCTCCTTCGATGCTCTCTCCGACTTCGCCAATTGGCTTCGAGG 60
Oy 85 ctacagcagatgctccacactcgcgcgcatgctgctcacatgacatcatgagtgagcatt 144
Db 61 CTCAGCGCATGCTCCACTTCGCGCGCATGTGCTCCACATGACATCATGATGATGGCATTT 120
Oy 145 ttgtccccaatttaactattggtcgctccagttattgaagtttgagaagacacaaagg 204
Db 121 TTGTCCCAATTTAACTATTGCGCTCCAGTTATGAAAGTTGAAGAACACACAAAGG 180
Oy 205 cataattgtagtgcacctatgattacaaatcctcttgattatgtctgaaccttgcaa 264
Db 181 GATATTGGATTTGTCACCTTATGTTACAAATCTCTTGATTATGTTGAGCCCTTGGCAA 240
Oy 265 aagctggtgcttcgtgtttacatttcacgttagagacatcaaaagataactgtgaagaac 324
Db 241 AACCTGCTGCTCTGTTTACATTTCATGTAGACATCAAAAGATTAACCTGGGAAGAAC 300
Oy 325 ttatccaagaatcaagtcacatgcatgattctctggttgagatcaagcctggagacc 384
Db 301 TTATCCAAAGATCAAGTCACATGATGATGCTCTGCTGTAGCATTTAAACCTGGAGACC 360
Oy 385 ccgt 388
Db 361 CCAT 364

RESULT 4
BG316079 374 bp mRNA linear EST 28-NOV-2001
LOCUS sak65g09.y1 Gm-cl043 Glycine max cDNA clone GENOME SYSTEMS CLONE
DEFINITION ID: Gm-cl043-4170 5' similar to TR:Q9SE42 Q9SE42
D-RIBULOSE-5-PHOSPHATE 3-EPIMERASE ; mRNA sequence.
ACCESSION BG316079
VERSION BG316079.1 GI:13125509
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 374)
Shoemaker,R., Kelm,P., Vodkin,L., Erpelting,J., Corryell,V., Khanna
,A., Bolla,B., Matra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800

```

Fax: 314 286 1810
 Email: estewatson.wustl.edu
 This clone is available through: ResGen, Invitrogen Corp. 2130
 South Memorial Parkway Huntsville, AL 35801 For further information
 call: (800)-553-4363 or contact via email: coudresgen.com
 High quality sequence stop: 351.

FEATURES

source

1..374
 Location/Qualifiers
 /organism="Glycine max"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl043-4170"
 /clone_1ib="Gm-cl043"
 /tissue-type="hypocotyl and plumule, germinating seeds"
 /lab_host="DH10B"
 /note="Vector: p773Pac (Pharmacia); Site_1: EcoRI;
 Site_2: NotI; This cDNA library was constructed from mRNA
 isolated from hypocotyl and plumule tissues of seeds
 germinated for three days of the cultivar Williams.
 Complementary DNA was synthesized from mRNA using a primer
 consisting of a poly(dT) sequence with a NotI restriction
 site. EcoRI adapters were ligated to the blunt-ended cDNA
 fragments followed by digestion with EcoRI and NotI. The
 EcoRI-NotI restriction site of the p773-Pac vector. The
 ligated cDNA fragments were transformed into DH10B host
 cells (Gibco BRL). This library was constructed by Dr.
 Randy Shoemaker."

BASE COUNT 104 a 80 c 89 g 101 t
 ORIGIN

Query Match

Best Local Similarity 87.2%; Score 338.2; DB 10; Length 374;

Matches 343; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 agaagaagaagaatggaatgacacggaagaatgctccttcgatgctcttcgcgac 62
 Db 24 AGAAGAAGAAGATGGAGTGGAGTGCACCGAAATTCCTCCTCGATGCTCTTCCGAC 83
 Qy 63 ttgcgaattggtcttcgaggtcagcgatgctccttcgagcgcgatggtccac 122
 Db 84 TTCGCCAATTGGCTTCGAGGCTCAGCGCATGCTCCACTTCGGCGCGATGGCTCCAC 143
 Qy 123 atgacatcatgcatggaatggtccttcctcccaatttaactatgagcgctcgaattatgaa 182
 Db 144 ATGACATCATGATGGGCAATTGTCCTCCCAATTAACTATTGGCGCTCCAGTTATTGAA 203
 Qy 183 agttgagaagaagcacaaagcatttgatgtcaacctatggtlacaacatcctct 242
 Db 204 AGTTGAGAAAGCACAAAGGATATTGATGATGTCACCTTATGATTACAAATCCCTCTT 263
 Qy 243 gataatgtgaacctgtgcaaaagctggtctctggtttacatttcattttcattgtagagaca 302
 Db 264 GATTATGTTGAGCCCTGGCAAAAGCTGGTCTTCTGTTTTCATTTCATTTGATGAGAGACA 323
 Qy 303 tcaaaagataacgcggaagaactatccaaagaatcaagtcacatggtcatg 353
 Db 324 TCAAAAGATACTGGGAAAGACTTATCCAAAGATCAAGTCACATGCGCANG 374

RESULT 5

AV412302 403 bp mRNA linear EST 23-MAY-2000
 LOCUS AV412302 Lotus japonicus young plants (two-week old) Lotus
 DEFINITION japonicus cDNA clone MM217c10_r 5', mRNA sequence.
 ACCESSION AV412302
 VERSION AV412302.1 GI:7741466
 KEYWORDS EST.

ORGANISM

Lotus japonicus.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae;

REFERENCE

1 (bases 1 to 403)
 AUTHORS Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
 TITLE Generation of 7137 non-redundant expressed sequence tags from a
 legume, Lotus japonicus
 JOURNAL DNA Res. 7 (2), 127-130 (2000)
 MEDLINE 20277479

COMMENT

Contact: Yasukazu Nakamura
 The First Laboratory for Plant Gene Research
 Kazusa DNA Research Institute
 Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
 Email: ynakem@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

FEATURES

source

1..403
 Location/Qualifiers
 /organism="Lotus japonicus"
 /db_xref="taxon:34305"
 /clone="MM217c10_r"
 /clone_1ib="Lotus japonicus young plants (two-week old)"
 /dev_stage="young plants (two-week old)"
 /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
 XhoI; Isolate=Miyakojima MG-20"

BASE COUNT 113 a 93 c 91 g 106 t
 ORIGIN

Query Match

Best Local Similarity 82.7%; Score 320.8; DB 9; Length 403;

Matches 340; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 4 gaaagaagaagaatggaatgacacggaagaatgctccttcgatgctcttcgcgact 63
 Db 32 GTAACAACAAAGATGGAGTGCACCCAAATTCCTCGTCATGCTTCATCGGACT 91
 Qy 64 ttgcgaattggtcttcgaggtcagcgatgctccttcgagcgcgatggtccaca 123
 Db 92 TCCCAATTGGCTTCGAGGCTCAACGCATGCTGATTATGCGCCGATGGCTCCACA 151
 Qy 124 tggacatcatgcatggtgcaattgtccccaatttaactatgagcgctcagttatgaa 183
 Db 152 TGGACATCATGATGGGCACTTGTGCCCAATTAACTATTGCGACTCGGCTCATGAAA 211
 Qy 184 gtttggagaagacacaaagcatttgatgtcaacctatggtlacaacatcctctg 243
 Db 212 GTTTGGAAGACACAAAGGCATATCTGATGTCACCTTATGATTCAAAATCCTCTTG 271
 Qy 244 attatgtgaacctgtgcaaaagctggtctctcgtgttcaactttacagtagagacat 303
 Db 272 ATTATGTTGAGCCTTTGGGAAGACAGTGCTTCTGCTTTTACATTTCATGATAGGCGAT 331
 Qy 304 caaagaataactcgtgaagaactatccaaagaatcaagtcacatgcatgcatggtg 363
 Db 332 CAAAAGATTAACGTGAAAGATTATCCAAAGATTAAAGTACAGGCGATGAAGCTGTG 391
 Qy 364 tagcatiaagc 375
 Db 392 TAGCATTTAAAGC 403

RESULT 6

AI442690 405 bp mRNA linear EST 28-NOV-2001
 LOCUS AI442690
 DEFINITION sa85b04.y1 Gm-cl004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
 Gm-cl004-6056 5' similar to TR:014105 O14105 RIBULOSE-PHOSPHATE
 3-EPIMERASE.; mRNA sequence.
 ACCESSION AI442690
 VERSION AI442690.1 GI:4297942
 KEYWORDS EST.

ORGANISM

soybean.
 Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.

REFERENCE 1 (bases 1 to 405)
AUTHORS Shoemaker, R., Keim, P., Vockin, L., Expelding, J., Corvelli, V., Rhanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shih, T., Jackson, Y., Cardenas, M., McCann, R., Waterson, R. and Wilson, R.
TITLE Public Soybean EST Project
JOURNAL Unpublished (1989)
COMMENT Contact: Shoemaker R./Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 923 Std Error: 0.00
Seq primer: -40RP from Gldco
High quality sequence stop: 395
POLYA-No.

FEATURES
Source location/Qualifiers
1..405 /organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl004-6056"
/clone_11b="Gm-cl004"
/tissue_type="root"
/lab_host="Xh10-Gold"
/note="Vector: plasmidscript II XR; Site_1: EcoRI; Site_2: XhoI; Root cDNA. The mRNA was isolated from entire roots of 8 day old 'Williams' seedlings which were propagated on paper towels with distilled water. Stratagene's cDNA Synthesis Kit (catalog #200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA is hemethylated. Stratagene's first-strand synthesis primer was used (GGAGAGAGAGAGAGAGACACTGCTCGAG(T)-18). After second-strand synthesis, the cDNA ends were 'polished' with clone Pfu DNA polymerase, ligated to EcoRI adapters, and phosphorylated. The XhoI site within the first-strand synthesis primer was restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GidcoBRL Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into Stratagene's plasmidscript II XR Predigested vector (plasmidscript II SR(+)) that had been digested with EcoRI and XhoI, and phosphorylated. Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts. Blue colonies 9n-15) have been sequenced, and possess putative cDNA inserts. This library was constructed by Dr. Paul Keim & Virginia H. Corvelli, Department of Biology, Box5640, Northern Arizona University, Flagstaff, AZ 86011, Phone: 520-523-1078 (Dr. Paul Keim), 520-523-1372 (Virginia H. Corvelli), Fax: 520-523-7500, email: paul.keim@na.u.edu, virginia.corvelli@na.u.edu"

BASE COUNT 111 a 86 c 96 g 112 t
ORIGIN

Query Match 80.0%; Score 310.4; DB: 9; Length 405;
Best Local Similarity 91.6%; Pred. No. 5.9e-79;
Matches 348; Conservative 0; Mismatches 11; Indels 21; Gaps 1;

9 aaagaagaagatgggaatcacacgcgaataatgactccttgatgctcttcgcagatgcgc 68
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 AAAGGAAGGATGGGAGTACACCGAAATTCCTCTTGATGAGCTCTCTTCGACTTCGCC 60

69 aattgcttcgcagagctcagcagatgctccacttcgcgcgcgattgtgtccacatgac 128

REFERENCE	TITLE	JOURNAL	COMMENT
129	alcatalgattggcatttgcctcccaatttaactaltgagcgtccagttatgaaagtty		
100	atcattgattggcatttgcctcccaatttaactaltgagcgtccagttatgaaagtty		
189	agaagaacacaaagcatttgcattgttcaacctatcgattgaacaaaccttattat		
160	agaaaagacacaaagcatttgcattgttcaacctatcgattgaacaaaccttattat		
249	gttgaaccttggcacaagcttgccttccttgcgttlttaactlttcaagtagaagacacaaa		
220	gtttgagcccttggcacaagccttgccttccttgcgttlttcaactlttcaagtagaagacacaaa		
309	gataacttggaaaagaactatcccaagaatcaagtcacatgacatgattccctggtttagca		
280	gataacttggaaaagaactatcccaagaatcaagtcacatgacatgattccctggtttagca		
369	ttaaagccttggagacccctt 388		
340	tttaagccttggagacccctt 359		
7	574 bp	linear	EST 20-JUL-2001
B1308956	B1308956	574 bp	linear
LOCUS	EST530366	GP0D Medicago truncatula	CDNA clone gpPD-10A22 5' end,
DEFINITION	EST530366	GP0D Medicago truncatula	CDNA clone gpPD-10A22 5' end,
ACCESSION	B1308956		
VERSION	B1308956.1	GI:14983283	
KEYWORDS	EST.		
SOURCE	barrel medic.		
ORGANISM	Medicago truncatula		
AUTHORS	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
	Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;		
	Medicago.		
	1 (bases 1 to 574)		
	Grusak, M.A., Samac, D.A., Town, C.D., Van Aken, S., Utterback, T., Cho		
	J. and Fraser, C.M.		
	ESTs from developing reproductive tissues of Medicago truncatula		
	Unpublished (2001)		
	Contact: Michael A. Grusak		
	USDA/ARS Children's Nutrition Research Center		
	Baylor College of Medicine		
	1100 Bates Street, Houston, TX 77030-2600, USA		
	Tel: 713-798-7044		
	Fax: 713-798-7078		
	Email: mgrusak@bcm.tmc.edu		
	B395811e		
	tiger sequence name: MTOA211TK		
	More information is available at: www.medicago.org		
	Seed primer: SKmod (CTA gaa cta gta gat cc).		
	Location/Qualifiers		
	1..574		
	/organism="Medicago truncatula"		
	/cultivar="A17"		
	/db_xref="taxon:3880"		
	/clone="gpPD-10A22"		
	/clone_1db="GP0D"		
	/tissue_type="Immature pod walls"		
	/dev_stage="Immature pods, ranging in age from 15 to 30		
	days after pollination"		
	/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:		
	XhoI; Immature pods, ranging in age from 15 to 30 days		
	after pollination, were collected from greenhouse-grown		
	plants. At harvest, seeds were removed from pods and		
	isolated pod walls were collected and immediately frozen		
	in liquid nitrogen. Pod walls were pooled for mRNA		
	extraction. cDNA was prepared from polyA+ enriched RNA.		
	The cDNA was directionally ligated into the Unizap XR		
	vector from Stratagene and packaged using GigaPack III		

Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XL04R cells."

BASE COUNT

183 a 110 c 131 g 150 t

ORIGIN

Query Match Best Local Similarity 79.3%; Score 307.8; DB 10; Length 574; Matches 336; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

6 aagaagaagaatgggaatgacacggaataatgctcctcgtatgctcctcgtacac 65
 32 AAAGAGAGAAAGATGGAGTACACGGAATAATGCTCCTTCATGCTATCATCATTTT 91
 66 gcaatttgcttcgagcgagcgatgcacgtcgcgtcgcgtcgcgtcgcgtcgc 125
 92 GCTAATTTGGCTTCGACAGCTCATGATCATTTACGGCGTGAATGGCTTCACATG 151
 126 gacatcgtatgagtgatcttcccaatttaactatgagcgctcgcgtatgaaagt 185
 152 GATATCATGATGGCATTTTGTCTTAACTAATTAAGCGCGCTCCATCATTTGAAGT 211
 186 ttgagaagaacacaaaggacatattgattgacacgtatgattacaatcctctgat 245
 212 TTGAGAAAGCACACAGAGGCAATCTGACGCTACCTGATGATTAACAAATTCATTGAT 271
 246 tatgtgaaccttgcaaaagcgtggtctcgttcaattcaattcagtcagtagacata 305
 272 TATGTTGAACCTTTGGGAAAGCTGGTCTTGTGTTTACATTTTCAATTAAGACATCA 331
 306 aagaataactggaagaactatccaaagaatcaagacatgacatgacatgacatg 365
 332 AAAGCAACTGGAAAGAACTTATCCAAATATTAAAGTACACGCGCATGAGCGCTGTGTA 391
 366 gcaataaagccttgagccccgt 388
 392 TCGATTAAGCCTGGAACATCCGT 414

RESULT 8

LOCUS

AM682881 641 bp mRNA linear EST 15-JUN-2000

DEFINITION NF001C10LF1081 Developing leaf Medicago truncatula cDNA clone

ACCESSION AM682881

VERSION AM682881.1 GI:7557597

KEYWORDS

SOURCE

ORGANISM

barrel medic.

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;

Medicago.

1 (bases 1 to 641)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Tel: 580 221 7391

Fax: 580 221 7380

Email: gdmay@noble.org

Insert Length: 641

Plate: 001 row: C column: 10

Seq primer: TCACACAGGAAACACCTATGAC.

Location/Qualifiers

1..641

/db_xref="taxon:3880"
 /clone="NF001C10LF"
 /clone_1lb="Developing leaf"
 /tissue_type="leaf"
 /dev_stage="Pooled developmental"
 /note="Vector: Lambda zap; Contains a mixture of very young, developing, mature and senescing leaves."

BASE COUNT 201 a 130 c 139 g 171 t

Query Match Best Local Similarity 79.3%; Score 307.8; DB 9; Length 641; Matches 336; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

6 aagaagaagaatggaatgacacggaataatgctcctcgtatgctcctcgtacac 65
 126 AAAGAGAGAAAGATGGAGTACACGGAATAATGCTCCTTCATGCTATCATCATTTT 185
 66 gcaatttgcttcgagcgagcgatgcacgtcgcgtcgcgtcgcgtcgcgtcgc 125
 186 GCTAATTTGGCTTCGACAGCTCATGATCATTTACGGCGCTGATTTGGCTTCACATG 245
 126 gacatcgtatgagtgatcttcccaatttaactatgagcgctcgcgtatgaaagt 185
 246 GATATCATGATGGCATTTTGTCTTAACTAATTAAGCGCGCTCCATCATTTGAAGT 305
 186 ttgagaagaacacaaaggacatattgattgacacgtatgattacaatcctctgat 245
 306 TTGAGAAAGCACACAGAGGCAATCTGACGCTACCTGATGATTAACAAATTCATTGAT 365
 246 tatgtgaaccttgcaaaagcgtggtctcgttcaattcaattcagtcagtagacata 305
 366 TATGTTGAACCTTTGGGAAAGCTGGTCTTGTGTTTACATTTTCAATTAAGACATCA 425
 306 aagaataactggaagaactatccaaagaatcaagacatgacatgacatgacatg 365
 426 AAAGCAACTGGAAAGAACTTATCCAAATATTAAAGTACACGCGCATGAGCGCTGTGTA 485
 366 gcaataaagccttgagccccgt 388
 486 TCGATTAAGCCTGGAACATCCGT 508

RESULT 9

LOCUS

BG455207 654 bp mRNA linear EST 19-MAR-2001

DEFINITION NF102610PL1082 Phosphate starved leaf Medicago truncatula cDNA

ACCESSION BG455207

VERSION BG455207.1 GI:13378532

KEYWORDS

SOURCE

ORGANISM

barrel medic.

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;

Medicago.

1 (bases 1 to 654)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Tel: 580 221 7325

Fax: 580 221 7380

Email: mjharrison@noble.org

Insert Length: 654

Std Error: 0.00

Plate: 102 row: G column: 10

Seq primer: TCACACAGGAACAGCTATGAC

FEATURES	Location/Qualifiers
source	1. .654

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/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF102G10PL"
/clone_lib="Phosphate starved leaf"
/lssue_type="leaf"
/dev_stage="trifoliolate"
/note="Vector: Lambda Zap; At the trifoliolate stage, M.
truncatula plants were transplanted to phosphate-free sand
and grown for a further 30 days. During this 30 day
period, the plants were fertilized twice weekly with 1/2
Hoslands solution containing only 20um potassilum
phosphate. RNA was prepared from above ground tissues."
BASE COUNT      202 a      136 c      143 g      172 t
ORIGIN

```

Query Match	79.3%	Score 307.8;	DB: 10;	Length 654;
Best Local Similarity	87.7%	Pred. NO. 3.9e-78;		
Matches 336;	Conservative	0;	Mismatches 47;	Indels 0;
				Gaps 0;

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Query Match      79.38; Score 307.8; DB 10; Length 654;
PostgreSQL 8.3.7 on i386-pc-linux-gnu, compiled by gcc 4.2.3 20060426, 64-bit
```

Best Local Similarity	87.78	Pred. NO. 3.9e-18
Matches 336	Conservative 0	Mismatches 47
		Indels 0
		Gaps 0

Db	117	AAAAGAAGAAAGATGGGAGAGTACACCGAAATATACCTCTCGATGATCATCATGATTTT	176
QY	66	ggcaatttgcttcgcggaggtcagcgcaatgctccactctggcgccgatttgctccacatg	1253
Db	177	GCTAATTTGGCTTCCGAGAGCTCATCGTATCATCATTAATTCAGCGCGCTGATTGGCTTCACATG	236
QY	126	gacatcatgtagtggacatttgctcccaatttaactcttggcgctccagttatgtaaagt	185
Db	237	GATATCATATGATGGGCAATTTGTCCTAATTTAACTATGGGCGCTCCAAATCATTTGAAAGT	296
QY	186	tttgaagaagcacacaagaagacatcttgatctgtccacttatggttacaatccctctgat	245
Db	297	TTTGGAAGAAGCACACAGAGGCGCATATCTGAGACTGTACCTGATGGTTACAAATTCACCTTGAT	356
QY	246	tatgttgaacctctgycaaaagctgctgctctctgcttgcatttcaattccagtagaagatca	305
Db	357	TATGTTCAACCTTTGGGAAAAAGCTGGTGGCTTCCTGTTTACATTTTCATATAGAGACATCA	416
QY	306	aaagataactcggaaagaacttatccaaagaatcaagtcacatgcatgcatgcatctcgtgtgta	365
Db	417	AAAGACACACTGGAAAGAACTTATCCAAAAATTTAAAGTCACACGCGATAGAGCGCTGGGTGA	476
QY	366	gcattaagcctggagaccccgct	388
Db	477	TTCGTAATAAGCCTGGAAACATCCGCT	499

RESULT 10	LOCUS	DEFINITION
BF645593	683 bp mRNA	linear EST 20-DEC-2000
	NF016H02C1P1027	Elicited cell culture Medicago truncatula cDNA
	clone NF016H02EC 5',	mRNA sequence.

REFERENCE	1 (bases 1 to 683)
AUTHORS	Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.
TITLE	Expressed Sequence Tags from the Samuel Roberts Noble Foundation - Center for Medicago Genomics Research
JOURNAL	Unpublished (2000)
COMMENT	Contact: Dixon RA

Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
Email: radix@noble.org
Insert length: 683 Std Error: 0.00
Plate: 016 row: H column: 02
Seq primer: TCACACAGGAAACACACTTGC.

FEATURES	Location/Qualifiers
source	1. .683

ORIGIN

Query Match	79.38;	Score 307.8;	DB 10;	Length 683;
-------------	--------	--------------	--------	-------------

Best Local Similarity 87.7%; Pred. NO. 4e-78;
Matches 336; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY	6	aagaaagaagaatgagggaatgaacccgaataatgctcttcagatgctcttcacgactc	65
Db	125	AAAAGAGAGAAAGATGGGAGTGAACACCGAAAATAGCTCTTCGTGATGCTATGATCAGATTTT	184
QY	66	gccaatctgcttcgcagagctcgaagatgctccacttcggcgcgcatcttgctccacatg	125
Db	185	GCTATTTGGCTTCCGAAGCTCATGCTATGATCAATTAACGCGCTGATTTGGCTTCACATG	244
QY	126	gaactcatagatgggcaattttgtccccaatttaactctttggcgctccagttattgaaagt	185
Db	245	GATATCATGATGGGCGATTGGTCCCTAAATTTAACTATGGGCGCTCCAAATCATTTGAAAGT	304
QY	186	tttgaagaagcacacaagaagcatalcttgatctgcatcttaattgttacaactccctctgac	245
Db	305	TTTGAGAAAGGCAACAGAGGCTATCTTGAGCTGTACCTCGATGGTTACAAATTCACCTTGAT	364
QY	246	tatgttgaaccttggcaaaagctgtgtcttcgtgtttacatttcaatccagtagaagacata	305
Db	365	TATGTGAACTTTGGGAAAAGCTGTGGTCTCTGTTTACATTTCTATATAGAGACATCA	424
QY	306	aaagataacttggaaagaacttatccaaagaatcaatgaatcaatgcatgcatgattcctgtgtta	365
Db	425	AAAAGACAACCTGGAAAGAACTTATCCAAAATATTAAGTCAACAGCGCATGAGCGCTCGGTGA	484
QY	366	gcattaaagcttggagcccccgt	388
Db	485	TCGATAAAGCCTGGACATCTCGT	507

RESULT	11
BG451782	
LOCUS	BG451782 597 bp mRNA linear EST 16-MAR-2001
DEFINITION	NF094004PTD1P1031 Drought Medicago truncatula cDNA clone NF094D04DT 5' , mRNA sequence.

ORGANISM
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;

Medicago.
1 (bases 1 to 597)
Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
Flores,H.R., Imman,J.T., Weller,J.W. and May,G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula drought library
Unpublished (2000)
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 597 Std Error: 0.00
Plate: 094 row: D column: 04
Seq primer: TCACACGGAACACGCTATGAC.
Location/Qualifiers
1. 597
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF094D04DT"
/clone.lib="Drought"
/tissue.type="Plantlets"
/dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap: Contains a mixture of entire
plantlets harvested in a series of days-post-watering
timepoints."
BASE COUNT 188 a 115 c 135 g 154 t 5 others
ORIGIN
Query Match 76.5%; Score 296.8; DB 10; Length 597;
Best Local Similarity 87.5%; Pred. No. 5.7e-75;
Matches 336; Conservative 0; Mismatches 47; Indels 1; Gaps 1;
QY 6 aagaagaagaatggaatgacac-gaaatagctcttcgatgctcttcgactt 64
DB 42 AAAAGAAAGATGGAGTGAACCTGAAATAGCTCTTGATGCTATCAGATT 101
QY 65 cgcgaattggtcttcgagagctcagcgcatgctccacttcggcgcgatlggtccacat 124
DB 102 TGTATTTTGGCTCCGAAAGCTCATCGTATGATCAATTACGGCGCTGATGGCTTCACAT 161
QY 125 ggaacatcatgattggtcattgtcccaatttaactatlttggtcgtccagtattgaag 184
DB 162 GGATATCATGATGGGCAATTGTCCCTAATTAACTATGGCGCTCCATCATTTGAAAG 221
QY 185 ttgggaagacacaaaggcatattgattgttcaccttaaggtaaacatcccttga 244
DB 222 TTGGAAGACACAGAGCATATCTGACTGCTCAGTGTGATGATCAATTGAAATCCACTTGA 281
QY 245 ttatgtgaaccttggaagaagctggtctgcttcatttcaatcagtaagaacatc 304
DB 282 TTATGTGAACCTTTGGAAAAAGCTGTGCTTCTTGTTTACATTATATAGAGCAATC 341
QY 305 aaagataactcggaaagaactatccaaagaatcaagtcacatgcatgcatcttggtgt 364
DB 342 AAAAGACACAGGAAAGCACTTATCCAAATATTAAGTACACAGCATAGAGCCTGTGT 401
QY 365 agcatlaagccttggaacccctt 388
DB 402 ATCGATTAAGCCTGGAAACATCCGT 425

RESULT 12
BE325053 613 bp mRNA linear EST 21-DEC-2000
LOCUS NF119G01STP1006 Developing stem Medicago truncatula cDNA clone
DEFINITION NF119G01ST 5', mRNA sequence.
ACCESSION BE325053
VERSION BE325053.2 GI:11935879
KEYWORDS EST.

SOURCE
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 613)
He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
,C.J., Flores,H.R., Imman,J.T., Weller,J.W., May,G.D. and Dixon
,R.A.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula stem library
Unpublished (2000)
On Jul 14, 2000 this sequence version replaced gi:9198914.
Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Medicago Genome Initiative accession: MGI:S:15815
Insert length: 633 Std Error: 0.00
Plate: 119 row: G column: 01
Seq primer: TCACACGGAACACGCTATGAC.
Location/Qualifiers
1. 613
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF119G01ST"
/clone.lib="Developing stem"
/tissue.type="stem"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap: Contains a mixture of
internodal stem segments"
BASE COUNT 186 a 125 c 134 g 168 t
ORIGIN
Query Match 76.5%; Score 296.8; DB 10; Length 613;
Best Local Similarity 87.5%; Pred. No. 5.8e-75;
Matches 336; Conservative 0; Mismatches 47; Indels 1; Gaps 1;
QY 6 aagaagaagaatggaatgacacgaaatagcttcgatgctcttcgactt 65
DB 104 AAAAGAAAGATGGAGTGAACGAAATAGCTCTTCATGCTATCAGATT 163
QY 66 gccaattggtcttcgagctcagcgcatgctccacttcggcgcatlggtccacatg 125
DB 164 GCTAATTTGGCTCCGAAGCTCATCGTATGATCAATTACGGCGCTGATGGCTTCACATG 223
QY 126 gacatcatgattggtcatttgcaccaatttaactatgggtcgcgattatgaagtc 185
DB 224 GATATCATGATGGGCAATTGTCCCTAATTAACTATGGCGCTCCATCATTTGAAAGT 283
QY 186 ttgagaagaacacaaaggcatattgattgtccaccttaagtgtataaacatcccttgat 245
DB 284 TTGGAAGACACAGAGCATATCTGACTGCTCAGTGTGATGATCAATCCACTTGAAT 343
QY 246 tatgtgaaccttggaagaagctggtctctctgttttaatttcaagtgaagaacatca 305
DB 344 TATGTGAACCTTTGGAAAAAGCTGTGCTTCTTGTTTACATTATATAGAGCAATCA 403
QY 306 aaagataactcggaaagaactatcc-aaagaatcaagtcacatgcatgcatcttggtgt 364
DB 404 AAAAGACACAGGAAAGCACTTATCCAAATATTAAGTACACAGCATAGAGCCTGTGT 463
QY 365 agcatlaagccttggaacccctt 388
DB 464 ATCGATTAAGCCTGGAAACATCCGT 487

RESULT 13

LOCUS	BF634692	666 bp	mRNA	linear	EST 19-DEC-2000
DEFINITION	BF634692	NF064B05D1P1044 Drought	Medicago truncatula	CDNA clone	NF064B05D1
ACCESSION	BF634692	5', mRNA sequence.			
VERSION	BF634692				
KEYWORDS	EST.				
SOURCE	barrel medic.				
ORGANISM	Medicago truncatula				
REFERENCE	1 (bases 1 to 666)				
AUTHORS	Torrez-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.				
TITLE	Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula drought library				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: May GD Plant Biology Division The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7391 Fax: 580 221 7380 Email: gdmay@noble.org Insert Length: 666 Std Error: 0.00 Plate: 064 row: B column: 05 Seq primer: TCACACAGGAACACGCTATGAC. Location/Qualifiers 1..666 /organism="Medicago truncatula" /db_xref="taxon:3880" /clone="NF064B05D1" /clone_lib="Drought" /tissue_type="Plantlets" /dev_stage="Pooled timepoints" /note="Vector: Lambda Zap; Contains a mixture of entire plantlets harvested in a series of days post-watering timepoints."				
FEATURES					
SOURCE					
BASE COUNT	189 a 127 c 165 g 182 t				3 others
ORIGIN					
Query Match	75.6%;	Score 293.2;	DB 10;	Length 666;	
Best Local Similarity	87.8%;	Pred. No. 6.5e-74;			
Matches 330;	Conservative 0;	Mismatches 45;	Indels 1;	Gaps 1;	
14	aaagttgggaatgaacacccggaataatgccccttcgtagtctcttcgcgacttcgccaattt	73			
2	AAAGATVGGAGATNNACCGAAATATAGCTCTTCGATGCTATCATCAGATTTTGTGCTAATTT	61			
74	gacttcgagagctcagcgcatgctccacttc-ggcgccgattggctccacatgagcatca	132			
62	GGCTTCCGAAGCTCATTCGTATGATTAATTTACGGCGCTGATTTGGCTTCAACATGAGTATCA	121			
133	tggaatgggcatttggctcccaatttaactatctgagcgctccagttatgaaagttgagaa	192			
122	TGGATGGGCATTTGTCCTTATTTAACTATGGGGCGCTCCCAATCATTTGAAATTTGAGAA	181			
193	agcacacaaaggcatatttgatgtgcaacctatggttaacaaatccctcttgattgtg	252			
182	AGCACACAGAGGCAATATGTGCACTGTCACTGATGCTTACAAATCCACTTGCATTATGTTG	241			
253	aaccttggcaaaagctgtgctcttgatttgaacttcaagttaagacatcaaaaagata	312			
242	AACCTTTGGGAACACTGCTGCTTGTTGTTTACATTTTCAATATTAAGACATCAAAAGACA	301			
313	actggaaagaaacttaccacaaagatcaagatcacatgcatgagattctgtgtgagcattaa	372			
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LOCUS
DEFINITION  AM348508 736 bp mRNA linear EST 04-OCT-2000
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              sequence.
ACCESSION  AM348508
VERSION    AM348508.1 GI:6846218
KEYWORDS
SOURCE
ORGANISM   Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
            1 (bases 1 to 736)
REFERENCE  Vokhin, L., Keim, P., Shoemaker, R., Retzel, E., Khanna, A., Coryell, V.,
            Epling, J., Ragh, C., Shoop, E., Pardinas, J., Liu, L. and Lewin, H.
            A Functional Genomics Program for Soybean (NSF 9872565)
            Unpublished (1999)
            Other ESTs: A1437973
            Contact: Vokhin, L.O., PI, A Functional Genomics Program for
            Soybean (NSF 9872565)
            Lewin, H. A., Director, Keck Center for Comparative and Functional
            Genomics
            University of Illinois
            Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
            Tel: (217) 244-6147
            Fax: (217) 333-4582
            Email: l-vokhin@uiuc.edu
            This clone is available through: Genome Systems, Inc. 4633 Woodl
            Parkway Circle St. Louis, Missouri 63134. For further information
            call: (800) 430-0030 or (314) 427-3324 FAX: (888) 919-3324 or (314)
            427-3324 or contact: clones@genomesystems.com or info@genome
            systems.com web site: www.genomesystems.com
            Seq primer: 5'-TTTTTTTTTTTTTTTTT(A/C/G)-3'.
FEATURES
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   /cultivar="Williams"
   /db_xref="taxon:3847"
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   /tissue_type="root"
   /lab_host="XLI0-Gold"
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XhoI; Library Gm-r1021 is a sequence-driven, rereaked set
of the original library Gm-cl004 which was prepared from
root cDNA. The mRNA was isolated from entire roots of 8
day old 'Williams' seedlings which were propagated on
paper towels with distilled water. Stratagene's cDNA
Synthesis Kit (catalog #200401) was used to synthesize
the cDNA. The Gm-cl004 library was constructed by Dr.
Paul Keim & Virginia H. Coryell, Department of Biology,
Box6640, Northern Arizona University, Flagstaff, AZ 86011,
email: paul.keim@nau.edu, virginia.coryell@nau.edu. The
contig analysis to select unique genes was performed by
the Laboratory of Ernest Retzel, Computational Biology
Centers, University of Minnesota,
http://www.cbc.umn.edu/ResearchProjects/Soybean/Index.html
. Rereaking was performed by Genome Systems, St. Louis,
http://www.genomesystems.com, and sequencing by the Keck
Center for Comparative and Functional Genomics,
University of Illinois,
http://www.life.uiuc.edu/biotech/keck.html."
BASE COUNT 197 a 164 c 131 g 215 t 29 others
ORIGIN
Query Match 73.6%; Score 285.4; DB 9; Length 736;

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Best Local Similarity 90.3%; Pred. No. 1.2e-71;
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Db 616 ACAAAAGCACAAAGGAGATTTGGATTGTCACTTATGGTTAACAATCCTGATTAT 557
QY 249 gttagaccttgcaaaagctgtgtctgtgtttacattcagctagacatcaaaa 308
|||||
Db 556 GTTAGACCTTGGCAAAAGCTGTGTCTGTGTACATTTCAATGAGACATCAAAA 497
QY 309 gataactggaagaactatcccaagaatcaagtcacatgagatgacatgagc 368
|||||
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QY 369 ttaagacctggagagcccccgt 388
|||||
Db 436 TTAAGCCTGGAGACCCCAT 417

RESULT 15

AV425192

LOCUS AV425192 399 bp mRNA linear EST 23-MAY-2000
DEFINITION AV425192 Lotus japonicus young plants (two-week old) Lotus

ACCESSION AV425192
VERSION AV425192.1 GI:7782868

KEYWORDS EST.
SOURCE Lotus japonicus.

ORGANISM

Lotus japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae;
Lotus.

REFERENCE 1 (bases 1 to 399)

Ashimizu, E., Nakamura, Y., Sato, S. and Tabata, S.
Generation of 7137 non-redundant expressed sequence tags from a
legume, Lotus japonicus

JOURNAL MEDLINE
DNA Res. 7 (2), 127-130 (2000)
20277479

COMMENT

Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakam@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/
Location/Qualifiers
1. 399

FEATURES

source

/organism="Lotus japonicus"
/db_xref="taxon:34305"
/clone="MM050b07_r"

/dev_stage="young plants (two-week old)"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; Isolate=Miyakojima MG-20"

BASE COUNT 104 a 103 c 83 g 109 t
ORIGIN

Query Match

72.5%; Score 281.2; DB 9; Length 399;
Best Local Similarity 91.4%; Pred. No. 1.6e-70;

Matches 298; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 4 gaaagaaagaaagatggaatgacacccgaatagctctcgatgctcttcgcgact 63
|||||

Db 74 gTAAACAACAAGCATGGAGTGACACCAAAATTGCTCGGATGCTCATCGAGCT 133
|||||

QY 64 tcgccaatctggtctcgaagctcagcagcagtcacatcctcggcgccgagttgctccaca 123
|||||
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QY 124 tggacatcatgagatgggcatcttctcccaactaactatgagcgtcccaagttatgaaa 183
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QY 184 gttagaagcaacaagaagcagcagcagtcagtcacatcagttatggttacaatcctctg 243
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QY 244 attatgttgaaccttggcaaaagctgtgtctctgtgtttacattcagctagagacat 303
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QY 304 caaagataactggaagaactatc 329
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Db 374 CAAAGATTAAGTGAAGAAAGATTATC 399

Search completed: July 3, 2002, 03:38:57
Job time: 43317 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 3, 2002, 07:57:38 ; Search time 796.36 Seconds

(without alignments)
836.510 Million cell updates/sec

Title: US-09-300-482-298

Perfect score: 388
Sequence: 1 ggagaaagaagaagatg.....ttaagcctggaccoccyt 388

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	225.2	58.0	1034	21	Arbidiopsis thalia
2	223.8	57.7	1153	21	Zea mays DNA fragm
3	222.4	57.3	910	21	Arabidopsis thalia
4	219.6	56.6	462	21	Zea mays DNA fragm
5	215.6	55.6	705	21	Pinus radiata ribu
6	215	55.4	508	21	Pinus radiata ribu
7	213.4	55.0	459	21	Pinus radiata ribu
8	211.6	54.5	410	21	Pinus radiata ribu
9	208	53.6	502	21	Pinus radiata ribu

10	204.2	52.6	620	21	Arbidiopsis thalia
11	154	39.7	1116	21	Arbidiopsis thalia
12	144	37.1	487	21	Zea mays DNA fragm
13	88.8	22.9	907	22	Human polynucleoti
14	88.8	22.9	1205	22	Human polynucleoti
15	88.8	22.9	2831	22	Human polynucleoti
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20	78.2	20.2	1379	23	Human polynucleoti
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31	68	17.5	3276	22	Human polynucleoti
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33	67.2	17.3	893	23	Human polynucleoti
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35	66.4	17.1	1437	23	Human polynucleoti
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ALIGNMENTS

RESULT 1

AC37136 standard; DNA: 1034 BP.

AC37136:

17-OCT-2000 (first entry)

Arbidiopsis thaliana DNA fragment SEQ ID NO: 16306.

Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

Arbidiopsis thaliana.

EP1033405-A2.

06-SEP-2000.

25-FEB-2000; 2000EP-0301439.

05-MAR-1999; 99US-0121825.

09-MAR-1999; 99US-0123180.

23-MAR-1999; 99US-0125788.

25-MAR-1999; 99US-0126264.

01-APR-1999; 99US-0126785.

06-APR-1999; 99US-0127462.

08-APR-1999; 99US-0128234.

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PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
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PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 58.0%; Score 225.2; DB 21; Length 1034;
Best Local Similarity 75.1%; Pred. No. 1.5e-61;
Matches 281; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

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DB 26 aagaagaatgtgtgcgcgaanaataagaccgttcgatgtcgcacgacttcgcaatcta 85
QY 75 gcttcgagagctcagcagctcctccacttcgcgcgcgacttgatgctccacatgacatg 134
DB 86 gcgcgcgagagccaatgcgatgacgatgttggcgcgaactgcgttcacatgagatattg 145
QY 135 gatggcatttgcctcccaacttaactattgcgcctccagttattgaagttagaanaag 194
DB 146 gacggcatttgcctccatcttaactatgcattgtgcctccgtcgcacgagattgcgaag 205
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QY 255 cccttgcaaaagctgtctcttgatttacaattcacaagtagagacatacaaaagataac 314
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DB 326 tggcaacaacttgcgcagaagattaaacttaactgcgtgatgagaccagcggtgctctaaag 385
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ID AAC44542 standard; DNA; 1153 BP.
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AC AAC44542;
XX
DT 18-OCT-2000 (first entry)
XX
DE Zea mays DNA fragment SEQ ID NO: 43215.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW Protein identification; signal transduction pathway; metabolic;
KW pathway; promoter; termination sequence; corn; ss.
XX
OS Zea mays subsp. mays.

XX
PN EPI033405-A2.
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PD
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PF 25-FEB-2000; 2000EP-0301439.
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XX 17-OCT-2000 (first entry)
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DE
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KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
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XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
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XX 06-SEP-2000.
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RESULT 4

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XX AAc43724;

DT 18-OCT-2000 (first entry)

DE Zea mays DNA fragment SEQ ID NO: 40278.

KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic;
KW pathway; promoter; termination sequence; corn; ss.

OS Zea mays subsp. mays.

PN EP1033405-A2.

PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

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PR 22-OCT-1999; 9905-0161404.
PR 25-OCT-1999; 9905-0161405.
PR 25-OCT-1999; 9905-0161406.
PR 26-OCT-1999; 9905-0161359.
PR 26-OCT-1999; 9905-0161360.
PR 26-OCT-1999; 9905-0161361.
PR 28-OCT-1999; 9905-0161920.
PR 28-OCT-1999; 9905-0161992.

PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 56.6%; Score 219.6; DB 21; Length 462;
Best Local Similarity 76.3%; Pred. No. 6.4e-60;
Matches 270; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

OY 26 gacacgaataagctcctcagatgctctcctccagatctcgaatttggtccgagc 85
Db 58 ggcgggaagatagcgccgtcgatgctctgctgagctttgcgaactcgtccgagc 117
OY 86 tcaagcgaatgctcgaactcgccgagcttggtccacatgacatcattgagtcatt 145
Db 118 tgaagcgaatgctcgcgcgaagcgccagcttgctacatgacatcattgagtcatt 177
OY 146 tgcgcccaatttaactatgtgcgcagatgattgaagcttgaagaagacacaaagc 205
Db 178 cgtcccaactgactatttggcgctcggtgacccaagccttgaggaacacacaaagc 237
OY 206 atatttgatgtacacttatgtgtacaatcctcctgtattatgttgaaccttgcaaa 265
Db 238 atatttgatgtacacttatgtgtacaagccttcagattacgtagaaccttttgaaa 297
OY 266 agctggtcctcgtgtttacattcacgtagaagacccaagaagacactggaaagac 325
Db 298 ggcggcgcttcggtatccattccatataagaagtgtcgaagacacacttggcaagatct 357
OY 326 tatccaaagatacaagtcacatgcatgattcctgtgtgtagcatataagccctgg 379
Db 358 catccaaagatacaagtcaggtatgctgctgtgtatcatctttagagccagc 411

RESULT 5
ID AAA67518
XX AAA67518 standard; DNA; 705 BP.

AC AAA67518;

DT 31-OCT-2000 (first entry)

DE Pinus radiata ribulose-phosphate-3-epimerase DNA SEQ ID NO:519.

KW Eucalyptus grandis; pinus radiata; Monterey pine; modification;
KW plant cell wall; polysaccharide; polysaccharide biosynthetic pathway;
KW transgenic plant; ds.

OS Pinus radiata.

PN WO200022092-A2.

PD 20-APR-2000.

PF 08-OCT-1999; 99WO-NZ00169.

PR 13-OCT-1998; 98US-0170862.

PR 11-AUG-1999; 99US-0148426.

PA (GENE-) GENESIS RES & DEV CORP LTD.

PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.

PI Bloksberg LN;

DR WPI; 2000-339328/29.

XX New genes encoding proteins involved in a plant polysaccharide
XX biosynthetic pathway, useful for modulating or altering the
XX polysaccharide content, composition or structure of the plant -
XX Claim 1; Page 205; 301pp; English.

CC The present invention describes isolated polynucleotides (PN) comprising
CC a sequence selected from one of 835 nucleotide sequences given in
CC AAA67073 to AAA67907, their (reverse) complements, sequences producing

CC an Expectation (E) value of 0.01 or less compared to the 835 sequences,
CC sequences at least 50% identical to them, 200, 100, 40 or 20-mers of the
CC 835 sequences or sequences that are degenerately equivalent or allelic
CC to the 835 sequences. The polynucleotides are used to modify the
CC activity of a polypeptide involved in a polysaccharide biosynthetic
CC pathway in the plant. They are especially used to modulate or alter the
CC polysaccharide content, composition or structure of the plant. AAB16268
CC to AAB16340 are proteins encoded by some of the polynucleotide sequence
XX given in the present invention.

SO Sequence 705 BP; 194 A; 137 C; 192 G; 182 T; 0 other;

Query Match 55.6%; Score 215.6; DB 21; Length 705;
Best Local Similarity 73.5%; Pred. No. 1.5e-58;
Matches 275; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

OY 9 aagaagaatgagatgacacccgaataatagctcctcagatgctctcgaactcgc 68
Db 132 aacacagaagaagggtatatacccttaaatltgtccgccaatgtgtcatcagacttgcg 191
OY 69 aatttgcttcgaaggctcagcgatgctccacttgcgcgcgatttgctccacatggac 128
Db 192 aatcgtgctcagaagcgcaaatatatacggaataatggtcgaattgtgtcatatggac 251
OY 129 atcatggttggtgacttttgcctccaatttaactatgtgcgctccagttattgaagtgtg 188
Db 252 atcatggttggtgacttttgcctccaatttaactatgtgcgacttgcagcttgcagtttg 311
OY 189 agaaagcacacaagaagcatatttgatgtcacttaagtattgataaactccttgattat 248
Db 312 aggaagcatatcccgagcatctcttgatgttcacactatgtgcacaaaccttggattat 371
OY 249 gtgaaccccttgcgaagaagcttgcctcgtgtttacatttcaagctagaagacataaa 308
Db 372 gtgaagcatttgcgaagaagcttgcagcttgcaggttcaacttcaatgtgaggtgcacaa 431
OY 309 gataactggaagaacttatcgaagaatcaagatcactatgcatgcatctcgtgtatga 368
Db 432 gacacttggcaagaatctcacaagaatcagaagaatgctgcatcgtgcgtgagtgagca 491
OY 369 ttaaagccttggac 382
Db 492 gtgaaccttggac 505

RESULT 6
ID AAA67512
XX AAA67512 standard; DNA; 508 BP.

AC AAA67512;

DT 31-OCT-2000 (first entry)

DE Pinus radiata ribulose-phosphate-3-epimerase DNA SEQ ID NO:513.

KW Eucalyptus grandis; pinus radiata; Monterey pine; modification;
KW plant cell wall; polysaccharide; polysaccharide biosynthetic pathway;
KW transgenic plant; ds.

OS Pinus radiata.

PN WO200022092-A2.

PD 20-APR-2000.

PF 08-OCT-1999; 99WO-NZ00169.

PR 13-OCT-1998; 98US-0170862.

PR 11-AUG-1999; 99US-0148426.

PA (GENE-) GENESIS RES & DEV CORP LTD.

PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.


```
RESULT 8
AAA67520
ID AAA67520 standard; DNA; 410 BP.
XX
AC AAA67520;
XX
DT 31-OCT-2000 (first entry)
XX
DE Pinus radiata ribulose-phosphate-3-epimerase DNA SEQ ID NO:521.
XX
KW Eucalyptus grandis; pinus radiata; Monterey pine; modification;
KW plant cell wall; polysaccharide; polysaccharide biosynthetic pathway;
KW transgenic plant; ds.
XX
OS Pinus radiata.
XX
PN WO200022092-A2.
XX
PD 20-APR-2000.
XX
PF 08-OCT-1999; 99WO-N200169.
XX
PR 13-OCT-1998; 98US-0170862.
XX
PR 11-AUG-1999; 99US-0148426.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
PI Bloksberg LN;
PI
XX
DR MPI; 2000-339328/29.
XX
PT New genes encoding proteins involved in a plant polysaccharide
PT biosynthetic pathway, useful for modulating or altering the
PT polysaccharide content, composition or structure of the plant -
XX
PS Claim 1; Page 206; 301pp; English.
XX
CC The present invention describes isolated polynucleotides (PN) comprising
CC a sequence selected from one of 835 nucleotide sequences given in
CC AAA67073 to AAA67907, their (reverse) complements, sequences producing
CC an expectation (E) value of 0.01 or less compared to the 835 sequences,
CC sequences at least 50% identical to them, 200, 100, 40 or 20-mers of the
CC 835 sequences or sequences that are degenerately equivalent or allelic
CC to the 835 sequences. The polynucleotides are used to modify the
CC activity of a polypeptide involved in a polysaccharide biosynthetic
CC pathway in the plant. They are especially used to modulate or alter the
CC polysaccharide content, composition or structure of the plant. AAB16268
CC to AAB16340 are proteins encoded by some of the polynucleotide sequence
CC given in the present invention.
XX
SQ Sequence 410 BP; 116 A; 80 C; 110 G; 104 T; 0 other;
```

```
Db 221 aggaagcataccagcattcttgatgtcatcttatgtccacaacctcttgattat 280
Qy 249 gttagaccttgcaaaagctgtctctgtttatattcactgtagacatacaaa 308
XX || || || || || || || || || || || || || || || || || || || ||
Db 281 gtggaacattctgcaaaagctgttagcttccacttctcatgtggaagctgcaaa 340
Qy 309 gataactggaagaactatcccaagaatcaagtcagtcagatctcctgtgtatga 368
XX || || || || || || || || || || || || || || || || || || || ||
Db 341 gacattggaagatctcatcaaaaagaatcgaatctgagctgagcctgagtgca 400
Qy 369 ttaagcctg 378
XX || || || || || || || || || || || || || || || || || || || ||
Db 401 gctgaacctg 410
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RESULT 9
AAA67513
ID AAA67513 standard; DNA; 502 BP.
XX
AC AAA67513;
XX
DT 31-OCT-2000 (first entry)
XX
DE Pinus radiata ribulose-phosphate-3-epimerase DNA SEQ ID NO:514.
XX
KW Eucalyptus grandis; pinus radiata; Monterey pine; modification;
KW plant cell wall; polysaccharide; polysaccharide biosynthetic pathway;
KW transgenic plant; ds.
XX
OS Pinus radiata.
XX
PN WO200022092-A2.
XX
PD 20-APR-2000.
XX
PF 08-OCT-1999; 99WO-N200169.
XX
PR 13-OCT-1998; 98US-0170862.
XX
PR 11-AUG-1999; 99US-0148426.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
PI Bloksberg LN;
PI
XX
DR MPI; 2000-339328/29.
XX
PT New genes encoding proteins involved in a plant polysaccharide
PT biosynthetic pathway, useful for modulating or altering the
PT polysaccharide content, composition or structure of the plant -
XX
PS Claim 1; Page 204; 301pp; English.
XX
CC The present invention describes isolated polynucleotides (PN) comprising
CC a sequence selected from one of 835 nucleotide sequences given in
CC AAA67073 to AAA67907, their (reverse) complements, sequences producing
CC an expectation (E) value of 0.01 or less compared to the 835 sequences,
CC sequences at least 50% identical to them, 200, 100, 40 or 20-mers of the
CC 835 sequences or sequences that are degenerately equivalent or allelic
CC to the 835 sequences. The polynucleotides are used to modify the
CC activity of a polypeptide involved in a polysaccharide biosynthetic
CC pathway in the plant. They are especially used to modulate or alter the
CC polysaccharide content, composition or structure of the plant. AAB16268
CC to AAB16340 are proteins encoded by some of the polynucleotide sequence
CC given in the present invention.
XX
SQ Sequence 502 BP; 138 A; 99 C; 138 G; 127 T; 0 other;
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Query Match 54.5%; Score 211.6; DB 21; Length 410;
Best Local Similarity 73.2%; Pred. No. 2.1e-57;
Matches 271; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
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Query Match 53.6%; Score 208; DB 21; Length 502;
Best Local Similarity 72.8%; Pred. No. 3.3e-56;
Matches 268; Conservative 0; Mismatches 100; Indels 0; Gaps 0;
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PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 05-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 06-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 09-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 10-AUG-1999; 99US-0147935.
PR 11-AUG-1999; 99US-0148171.
PR 12-AUG-1999; 99US-0148319.
PR 13-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 16-AUG-1999; 99US-0148684.
PR 17-AUG-1999; 99US-0149368.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 23-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 25-AUG-1999; 99US-0149930.
PR 26-AUG-1999; 99US-0150566.
PR 27-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 30-AUG-1999; 99US-0151080.
PR 31-AUG-1999; 99US-0151303.
PR 01-SEP-1999; 99US-0151438.
PR 07-SEP-1999; 99US-0151930.
PR 10-SEP-1999; 99US-0152363.
PR 13-SEP-1999; 99US-0153070.
PR 15-SEP-1999; 99US-0153758.
PR 16-SEP-1999; 99US-0154018.
PR 20-SEP-1999; 99US-0154039.
PR 22-SEP-1999; 99US-0154779.
PR 23-SEP-1999; 99US-0155139.
PR 24-SEP-1999; 99US-0155486.
PR 28-SEP-1999; 99US-0155659.
PR 29-SEP-1999; 99US-0156458.
PR 04-OCT-1999; 99US-0156596.
PR 05-OCT-1999; 99US-0157117.
PR 06-OCT-1999; 99US-0157753.
PR 07-OCT-1999; 99US-0157865.
PR 08-OCT-1999; 99US-0158029.
PR 12-OCT-1999; 99US-0158232.
PR 13-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 14-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159684.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
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PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161982.
PR 29-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.
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Query Match 52.6%; Score 204.2; DB 21; Length 620;
Best Local Similarity 74.0%; Pred. No. 6e-55;
Matches 276; Conservative 0; Mismatches 88; Indels 9; Gaps 1;

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QY 25 tgacacggaatatgccccttcgatatgctctctccgaactcgccaaattggtccgagg 84
D 5 tctgcgcgaataatagcacgcgtcgatctgtctacatcggaactcgcaatctagcgcggagg 64
QY 85 ctacgcgatgctccacatctcgcgccgatggtgcacatggaacatcatgagtg----- 138
D 65 ccaatcgatcgatcgatggtggtgcgtacactggtctacatggaatattatgagcgtcccc 124
QY 139 ---ggcatttgcctcccaattacactatggcgtccgaattatgaagttagaagaagc 195
D 125 gcaggcatttgcctcccaattacactatggcgtctcctctcatalcgaggttgcgaagc 184
QY 196 acacaaagcatattggaattgacacctatggttacaaatctcttataatgttggaac 255
D 185 acactatgatatcttgattggtcccaactatggttagcgaacccatgataatgattgcac 244
QY 256 ccttgcaaaagctggtctgtctgtttacatttcacgttagagaacaaagaataact 315
D 245 agatggtctaaagctgggtctgttctgtttcacattccacgtcgaggtgcccagaataat 304
QY 316 ggaagaagacttaccaaagaacatgacatgacatgacatgacatgacatgacatgac 375
D 305 ggcacaacttgcgagaagataaagtctactggatgagacacagcggcgtctctaaagc 364
QY 376 ctgggagccccct 388
D 365 ctggagacacctgt 377
Db 365 ctggagacacctgt 377

RESULT 11
AAC38028
ID AAC38028 standard; DNA; 1116 BP.
XX
AC AAC38028;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 19528.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
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PR 29-MAR-1999: 99US-0126785.
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PR 28-SEP-1999: 99US-0156458.
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PR 04-OCT-1999: 99US-0157117.
PR 05-OCT-1999: 99US-0157753.
PR 06-OCT-1999: 99US-0157865.
PR 07-OCT-1999: 99US-0158029.
PR 08-OCT-1999: 99US-0158232.

0.

PD	06-SEP-2000.	
XX		
PF	25-FEB-2000;	2000EP-0301439
XX		
PR	25-FEB-1999;	990US-0121895
PR	05-MAR-1999;	990US-0123180
PR	05-MAR-1999;	990US-0123548
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PR	25-MAR-1999;	990US-0126785
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PR	08-APR-1999;	990US-0128714
PR	15-APR-1999;	990US-0129845
PR	19-APR-1999;	990US-0130077
PR	23-APR-1999;	990US-0130540
PR	28-APR-1999;	990US-0130891
PR	30-APR-1999;	990US-0131449
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PR	01-JUN-1999;	990US-0136799
PR	03-JUN-1999;	990US-0137222
PR	04-JUN-1999;	990US-0137528
PR	08-JUN-1999;	990US-0137802
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PR	18-JUN-1999;	990US-0139492
PR		990US-0139454

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PF	25-FEB-2000.	2000EP-0310439
PR	25-FEB-1999.	990US-0121895
PR	05-MAR-1999.	990US-0123180
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PR	05-MAY-1999.	990US-0133484
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PR	25-MAY-1999.	990US-0135629
PR	27-MAY-1999.	990US-0136021
PR	28-MAY-1999.	990US-0136392
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PR	10-JUN-1999.	990US-0138540
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PR	16-JUN-1999.	990US-0139452
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PR	30-JUN-1999.	990US-0140991
PR	01-JUL-1999.	990US-0141887
PR	01-JUL-1999.	990US-0141842
PR	02-JUL-1999.	990US-0142154
PR	02-JUL-1999.	990US-0142054

CC polypeptide which is useful for treating a disease or condition
CC associated with decreased or increased expression of functional human
CC isomerase. ISOM polypeptides are useful for treating immune disorders
CC such as inflammation, acquired immunodeficiency syndrome (AIDS),
CC Addison's disease, adult respiratory distress syndrome (ARDS),
CC allergies, anemia, asthma, atherosclerosis, Crohn's disease, acropic
CC dermatitis, glomerulonephritis, Grave's disease, Hashimoto's
CC thyroiditis, multiple sclerosis, osteoporosis, rheumatoid arthritis,
CC psoriasis, myocardial or pericardial inflammation, and autoimmune
CC diseases, diabetes mellitus, cancers and cell proliferative
CC disorders such as actinic keratosis, prostatitis, cirrhosis, and
CC myelofibrosis.

XX Sequence 1205 BP; 331 A; 224 C; 291 G; 359 T; 0 other;

Query Match 22.9% Score 88.8; DB 22: Length 1205;
Best Local Similarity 56.9%; Pred. No. 5.6e-18;
Matches 206; Conservative 0; Mismatches 147; Indels 9; Gaps 2;

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QY 93 atgctccacttcggcgccgattggtcccaatgagacatgagatggagctttgcccc 152
DB 81 atgctagactctggggcgccgattatctgcacctggagcgtatgagcggcatttggctccc 140
QY 153 aatttaaccttgcgcctcagttatgaaatttgaagaagca-----cacaagaagca 206
DB 141 aacatcacttctggtacacctgtgtgtagaagaagccttcgaaagagcttaagccagacct 200
QY 207 tatttgagattgcacctatggtttacaacatcctctgattatgttgaaccttggcaaaa 266
DB 201 tctcttgacatcagacatgtagtgggtccaaagcagaacagtggttaagccaatggtgtga 260
QY 267 gctgtgcttcggtttcattcattccagtagacatcaaaagatactcggaaagacct 326
DB 261 gtagagagcaatcagtaacacattcctcagag--gctactgaagaccaggggctttg 317
QY 327 atccaaagaatcaagtcacatgcatgcatgctcctggtgtagcattaaagctggagcccc 386
DB 318 attaaagacatcgcggagagatggatgaaggttggccttcgcatcaaacaggaaacctca 377

OY 387 gt 388
DB 378 gt 379

RESULT 15
AA160513
ID AA160513 standard; cDNA; 2831 BP.

XX AA160513;

XX 22-OCT-2001 (first entry)

XX Human polynucleotide SEQ ID NO 4502.

XX Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokine; thrombolytic; drug screening; arthritis; inflammation;
XX leukaemia; ss.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US34263.

XX 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.

XX (HSE-) HSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

DR WPI: 2001-442253/47.
P-PSDB; AAA41357.

XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -

XX Claim 1; SEQ ID NO 4502; 10078bp; English.

CC The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AA158642-AA162213) with noctropic,
CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemia and
CC C.N.S. disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.

XX Sequence 2831 BP; 873 A; 476 C; 583 G; 897 T; 2 other;

Query Match 22.9% Score 88.8; DB 22: Length 2831;
Best Local Similarity 56.9%; Pred. No. 8.5e-18;
Matches 206; Conservative 0; Mismatches 147; Indels 9; Gaps 2;

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DB 73 aagattggccgcctccatccctcaacagcagccttgccaatttagggcgagtgctccgcg 132
QY 93 atgctccacttcggcgccgattggtcccaatgagacatagatggagctttgcccc 152
DB 133 atgctagactctggggcgccgattatctgcacctggagcagtagagcggcatttggctccc 192
QY 153 aatttaaccttgcgcctcagttatgaaatttgaagaagca-----cacaagaagca 206
DB 193 aacatcacttggtagacctgtgtagaagaagccttcgaaagagtagcagagacct 252
QY 207 tatttgagattgcacctatggtttacaacatcctctgattatgttgaaccttggcaaaa 266
DB 253 tctcttgacatcagacatgtagtgggtccaaagcagaacagtggttaagccaatggtgtga 312
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DB 313 gtagagagcaatcagtaacacattcctcagag--gctactgaagaccaggggctttg 369
QY 327 atccaaagaatcaagtcacatgcatgcatgctcctggtgtagcattaaagctggagcccc 386
DB 370 attaaagacatcgcggagagatggatgaaggttggccttcgcatcaaacaggaaacctca 429
QY 387 gt 388

Wed Jul 3 12:01:05 2002

us-09-300-482-298.rng

Page 18

Db 430 gt 431

Search completed: July 3, 2002, 07:57:43
Job time: 24418 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 3, 2002, 07:56:01 ; Search time 185.98 Seconds

(without alignments)
512.452 Million cell updates/sec

Title: US-09-300-482-298

Perfect score: 388
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Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	65.4	16.9	1234	4	US-08-858-207A-110
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4	58	14.9	1019	4	US-09-265-315-79
5	58	14.9	1019	4	US-09-265-315-79
6	58	14.9	1019	4	US-09-265-315-79
7	34	8.8	3781	3	US-08-688-988-5
8	31.6	8.1	40352	3	US-08-846-111D-15
9	31	8.0	1413	4	US-08-900-117A-3
10	31	8.0	1430	4	US-08-276-452A-25
11	31	8.0	1430	2	US-08-798-744-25
12	30.8	7.9	908	4	US-09-457-046B-17
13	30.6	7.9	3150	3	US-08-673-814-5
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16	30	7.7	2168	3	US-08-749-522-6
17	29.8	7.7	2622	1	US-08-766-014-23
18	29.8	7.7	5300	1	US-08-766-014-1
19	29.8	7.7	59065	4	US-09-813-817-3
20	29.6	7.6	911	4	US-09-457-046B-19
21	29.6	7.6	911	4	US-09-457-046B-21
22	29.6	7.6	1326	4	US-09-457-046B-53
23	29.4	7.6	1474	4	US-08-821-994-64
24	29.4	7.6	6960	2	US-08-841-349-3
25	29.4	7.6	8176	2	US-08-841-349-5
26	29	7.5	4182	1	US-07-973-257-1
27	29	7.5	5181	1	US-08-257-073-10

C 28	29	7.5	8700	2	US-08-392-625-16	Sequence 16, Appl
C 29	29	7.5	8700	2	US-08-466-961A-16	Sequence 16, Appl
C 30	28.6	7.4	15872	4	US-09-105-537-1	Sequence 1, Appl
C 31	28.4	7.3	1347	3	US-08-663-713A-1	Sequence 1, Appl
C 32	28.4	7.3	1347	3	US-09-014-888-1	Sequence 2, Appl
C 33	28.4	7.3	2835	1	US-08-750-533-2	Sequence 2, Appl
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C 35	28.4	7.3	4765	4	US-08-894-818B-7	Sequence 7, Appl
C 36	28.4	7.3	4765	4	US-09-445-472-5	Sequence 5, Appl
C 37	28.4	7.3	10207	1	US-08-920-812-2	Sequence 2, Appl
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C 40	28.4	7.3	10207	1	US-08-362-577C-2	Sequence 2, Appl
C 41	28.4	7.3	10207	2	US-08-920-828-2	Sequence 2, Appl
C 42	28.2	7.3	305	4	US-08-821-994-81	Sequence 81, Appl
C 43	28.2	7.3	753	4	US-08-861-774E-71	Sequence 71, Appl
C 44	28.2	7.3	924	4	US-09-105-390-33	Sequence 33, Appl
C 45	28.2	7.3	1035	4	US-09-105-390-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1
US-09-276-531-8
; Sequence 8, Application US/09276531
; Patent No. 6183968
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Hallman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Reddy, Roopa
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
; TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/276,531
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 60/079,677
; FILING DATE: March 27, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Lynn E. Murty, Ph.D.
; REGISTRATION NUMBER: 42,918
; REFERENCE/DOCKET NUMBER: PA-0008 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3556 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LIVERUT01

CLONE: 1753826
US-09-276-531-8

Query Match
Best Local Similarity 22.9%; Score 88.8; DB 4; Length 3556;
Matches 206; Conservative 0; Mismatches 147; Indels 9; Gaps 2;

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Db 132 ATGCTAAGCTCTGGGCGCAATTTCTGCACCTGGAGTAATGAGCGGCAATTTGCTCC 191
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Db 192 AACATCACCCTTGGTCACCTGTGTAGAAAGCCTTGAAGAGCAGTACGACGACCTT 251
QY 207 tatttgatttcacactatggttccaactcctctgtatgttgtaaccttgcaaaa 266
Db 252 TTCTTGAACATGCACATGATGTGTGCAAGCCAGAACAGTGGTAAAGCCATGGCTG 311
QY 267 gctgtgctctcgtgtttacatcttcaacgtagagacatcaaaagtaacttggaag 326
Db 312 GAGAGAGCCAACTGACCTACCTTTCATCTCGAG---GCTACTGAGAACCCAGGCGCTT 368
QY 327 atccaaagaatcaagtcacatgcatgatactcctggtgttagcatlaagcctggag 386
Db 369 ATTAAAGACATTGGAGAAATGAGTGAAGTTGGCTTGCATCAAAACGAGAACTCTCA 428
QY 387 gt 388
Db 429 GT 430

RESULT 2

US-08-858-207A-110
Sequence 110, Application US/08858207A
Patent No. 6348328

GENERAL INFORMATION:

APPLICANT: Black, Michael
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328e1 Compounds
NUMBER OF SEQUENCES: 552
CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA

ZIP: 19406-0939
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858, 207A
FILING DATE: 09-MAY-1997

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996

ATTORNEY/AGENT INFORMATION:
NAME: Gimm1, Edward R

REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50475

TELECOMMUNICATION INFORMATION:
NAME: Waitburg, Richard J.
REGISTRATION NUMBER: 32,327

TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090

INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 1234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-858-207A-110

Query Match
Best Local Similarity 16.9%; Score 65.4; DB 4; Length 1234;
Matches 126; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

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Db 1016 CTAGAACCACTGGGCGCAATATGCGCATATGATGATGATGATGATGATGATGATG 1075
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Db 1136 GATTGCCACTTGTATGTGTGTCAAACCTGACATCATCTGGAATAATT 1182

RESULT 3

US-08-714-918-79/C
Sequence 79, Application US/08714918
Patent No. 6037123

GENERAL INFORMATION:

APPLICANT: Benton, Bret
APPLICANT: Lee, Ving
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu

TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.

ZIP: 90071-2066
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714, 918
FILING DATE: September 13, 1996

CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995

ATTORNEY/AGENT INFORMATION:
NAME: Waitburg, Richard J.

REGISTRATION NUMBER: 32,327


```

MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Marburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 1019 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-79

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```

Query Match      14.9%; Score 58; DB 4; Length 1019;
Best Local Similarity 56.9%; Pred. No. 5.8e-10;
Matches 161; Conservative 0; Mismatches 118; Indels 4; Gaps 3;

QY 105 ggcgcgcagatggcctcacatgacatcatgagcatttgcctcccaatttaactat 164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1001 GGNTCGACGAGAGTTTGTATGATGATGATGATGATGATGATGATGATGATGAT 164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 165 ggcgcctcaatttgaagtttgagaagcacacaaggcatttgcctcccaatttgc 224
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 941 GGTTCACCAATATTGATGATGATGATGATGATGATGATGATGATGATGATGAT 224
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 225 atggtt-acaaatcccttgattatgtaaccccttgcaaaagctgctctc-9gtt 282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 881 ATGATTGAAAATTCAGAAAAGTATATTCATTCATTCAGAACATGTCGATATGAT 882
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 283 ttacattcaagtagagacatcaaaagataactggaagaactatcacaagaatcaagt 342
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 821 TTNCATTTGATGTCGAATCAACGCCCTCATTA--TTTCATCGTGTCTATTTCAATGATTAAAC 764
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 343 cacatggcatgtctcgtgtgtagatctaagcctggagccccc 385
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 763 ATTTAGATTAATAAAGCTGTGTGATTAATTAATTCCTGTACACC 721
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 6
US-09-266-417-79/C
Sequence 79, Application US/09266417
Patent No. 6228588
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Ving J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:

```

```

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/266,417
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Marburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/248
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 1019 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-266-417-79

```

```

Query Match      14.9%; Score 58; DB 4; Length 1019;
Best Local Similarity 56.9%; Pred. No. 5.8e-10;
Matches 161; Conservative 0; Mismatches 118; Indels 4; Gaps 3;

QY 105 ggcgcgcagatggcctcacatgacatcatgagcatttgcctcccaatttaactat 164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1001 GGNTCGACGAGAGTTTGTATGATGATGATGATGATGATGATGATGATGATGAT 164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 165 ggcgcctcaatttgaagtttgagaagcacacaaggcatttgcctcccaatttgc 224
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 941 GGTTCACCAATATTGATGATGATGATGATGATGATGATGATGATGATGATGAT 224
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QY 225 atggtt-acaaatcccttgattatgtaaccccttgcaaaagctgctctc-9gtt 282
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DB 881 ATGATTGAAAATTCAGAAAAGTATATTCATTCATTCAGAACATGTCGATATGAT 882
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QY 283 ttacattcaagtagagacatcaaaagataactggaagaactatcacaagaatcaagt 342
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 821 TTNCATTTGATGTCGAATCAACGCCCTCATTA--TTTCATCGTGTCTATTTCAATGATTAAAC 764
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 343 cacatggcatgtctcgtgtgtagatctaagcctggagccccc 385
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 763 ATTTAGATTAATAAAGCTGTGTGATTAATTAATTCCTGTACACC 721
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 7
US-08-688-986-5/C
Sequence 5, Application US/0868988B
Patent No. 6096545
GENERAL INFORMATION:
APPLICANT: Lefebvre, Daniel D.
APPLICANT: Malboob, Mohammad A.

```


NAME/KEY: SEQ ID NO.3
LOCATION: NA
IDENTIFICATION METHOD: By Similarity with Known Sequence
OTHER INFORMATION: Hypothetical RNA Promoter Sequence
PUBLICATION INFORMATION: NA
US-08-900-117A-3

Query Match
Best Local Similarity 8.0%; Score 31; DB 4; Length 1413;
Matches 46; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 135 gatggcatttgcaccaatttaactatctgcctccagttatgaagttgagaag 194
DB 714 GAAGTCAATTTTCGACAAATTAACTTGGCGCTGCTTTTCGCAAAATTGGCCCAAT 655
QY 195 cacacaagc 205
DB 654 TTCAAAATGC 644

RESULT 10
US-08-276-452A-25/c
Sequence 25; Application US/08276452A
Patent No. 5646029

GENERAL INFORMATION:
APPLICANT: Chen, Chao-Guang
APPLICANT: Mau, Shao-Lim
APPLICANT: Du, He
APPLICANT: Gane, Alison M
APPLICANT: Bacic, Antony
APPLICANT: Clarke, Adrienne E
TITLE OF INVENTION: Plant Arabinogalactan Protein (AGP) Genes
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: United States of America
ZIP: 80303

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,452A
FILING DATE: 18-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Caruthers, Jennie M.
REGISTRATION NUMBER: 34,464
REFERENCE/DOCKET NUMBER: 27-91A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303)499-8080
TELEFAX: (303)499-8089
TELEX: 49617824

INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:

LENGTH: 1430 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:

NAME/KEY: CDS
LOCATION: 2..1312
FEATURE:

NAME/KEY: misc-feature
LOCATION: 41..112

OTHER INFORMATION: /note= "Derived amino acid sequence
corresponding to the peptide sequence by protein

OTHER INFORMATION: microsequencing"
FEATURE:
NAME/KEY: misc-feature
LOCATION: 41..112
OTHER INFORMATION: /note= "Derived amino acids 14-24,
28, 30, 32-37 are identical to sequences obtained
OTHER INFORMATION: by protein microsequencing"
FEATURE:

NAME/KEY: misc-feature
LOCATION: 25..31
OTHER INFORMATION: /note= "Amino acids 25, 27, 29, and
OTHER INFORMATION: 31 are hydroxylated proline residues; amino acid
OTHER INFORMATION: 26 can be T instead of A"
US-08-276-452A-25

Query Match
Best Local Similarity 8.0%; Score 31; DB 1; Length 1430;
Matches 103; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 143 ttctcccaatttaactatgcctccagttatgaagttgagaagcacacaa 202
DB 992 TGTAGTCTCAGAGTAGCATGTGTTTGTGTGTAATCTCAGAGAAACATTTGT 933
QY 203 ggcatttgcattgcacctatggttacaaatcccttgatatagtgaacctggc 262
DB 932 TGTATTGTTTGTGTAATTCGAGAAACATTAATGTTGTGTAATTCGAGCA 873
QY 263 aaaaactgctcctgctgttaccattcacgtagagagactcaaaagaactgaaga 322
DB 872 AAGCATGTTGTTATTTGTTGTAATTCGAGAAACATTAATGTTGTGTAATTCG 813
QY 323 actatccaagaatcaagtcacatgacatgacatgacatgacatgacatgacat 365
DB 812 TGTATTCTCGAGAAACATTAATGTTATTTATTTGTTGTTGTA 770

RESULT 11
US-08-798-744-25/c
Sequence 25; Application US/08798744
Patent No. 5830747

GENERAL INFORMATION:
APPLICANT: Chen, Chao-Guang
APPLICANT: Mau, Shao-Lim
APPLICANT: Du, He
APPLICANT: Gane, Alison M
APPLICANT: Bacic, Antony
APPLICANT: Clarke, Adrienne E
TITLE OF INVENTION: Plant Arabinogalactan Protein (AGP) Genes
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: United States of America
ZIP: 80303

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,744
FILING DATE: 13-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/276,452
FILING DATE: 18-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Caruthers, Jennie M.
REGISTRATION NUMBER: 34,464
REFERENCE/DOCKET NUMBER: 27-91A

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 3, 2002, 05:12:38 ; Search time 5254.53 Seconds

(without alignments)
1091.224 Million cell updates/sec

Title: US-09-300-482-311

Perfect score: 274
Sequence: 1 ctccatctcttctccacc.....gccaaagatgcgcgcgcacgcg 274

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_da:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sv:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

1	81.4	29.7	798	8	AY066038	AY066038 Arabidops
2	81.4	29.7	959	8	AF360330	AF360330 Arabidops
3	81.4	29.7	1464	8	AY054172	AY054172 Arabidops
4	81.4	29.7	66653	8	AC016972	AC016972 Arabidops
5	81.4	29.7	84957	8	AC006200	AC006200 Arabidops
6	68	24.8	1118	6	A93589	A93589 Sequence 1
7	68	24.8	1118	6	SPR5P1R	L43068 Spinacia ol
8	62	22.6	1084	8	AF154658	AF154658 Nicotiana
9	54.6	19.9	135296	2	AP003944	AP003944 Oryza sat
10	54.6	19.9	136775	2	AP004279	AP004279 Oryza sat
11	54.6	19.9	150638	2	AP003616	AP003616 Oryza sat
12	54	19.7	998	8	AY045785	AY045785 Arabidops
13	54	19.7	93234	8	AC009465	AC009465 Arabidops
14	54	19.7	95310	8	ATAC011437	ATAC011437 Arabidops
15	49.2	18.0	454	6	AX172623	AX172623 Sequence
16	48.4	17.7	34158	1	SCR13	AL512667 Streptomy
17	47.6	17.4	152396	8	AP002971	AP002971 Oryza sat
18	47.6	17.4	163089	2	AP004358	AP004358 Oryza sat
19	47.4	17.3	37898	1	SCB34	AL353862 Streptomy
20	46.6	17.0	11727	1	AE008449	AE008449 Streptoco
21	46.6	17.0	36224	1	SCD78	AL034355 Streptomy
22	46.6	17.0	144561	2	SPNEU1905	AP004307 Oryza sat
23	46.6	17.0	297172	2	SPNEU1905	AL449927 Streptoco
24	46.4	16.9	1288	6	AR007563	AR007563 Sequence
25	46.4	16.9	161266	8	AR001278	AP001278 Oryza sat
26	45.8	16.7	3800	1	SAR416377	AJ416377 Streptomy
27	45.8	16.7	14916	1	AE005900	AE005900 Caulobact
28	45	16.4	10834	1	AE004020	AE004020 Xylella f
29	44.8	16.4	3875	1	RHPHAS	X66407 R. ruber ORF
30	44.6	16.3	15424	1	AE007019	AE007019 Mycobacte
31	44.6	16.3	40790	1	MTC1493	Z93844 Mycobacteri
32	44.6	16.3	77534	1	AF235504	AF235504 Streptomy
33	44.6	16.3	139399	8	AP002865	AP002865 Oryza sat
34	44.6	16.3	182756	8	AC007789	AC007789 Oryza sat
35	44.4	16.2	109980	1	AE005969	AE005969 Caulobact
36	44.4	16.2	43632	1	SC685	AL049485 Streptomy
37	44.4	16.2	190097	2	AC094543	AC094543 Rattus no
38	44.2	16.1	1593	1	AF113605	AF113605 Streptomy
39	44	16.1	2647	8	OSHPERG	X61280 O. sativa ge
40	44	16.1	28732	1	AF082100	AF082100 Streptomy
41	43.8	16.0	273	1	MTU13938	U13938 Mycobacteri
42	43.8	16.0	194415	2	AP004365	AP004365 Oryza sat
43	43.6	15.9	42273	8	NCB12N19	AL669987 Neurospor
44	43.6	15.9	69943	8	NCB11E6	AL442043 Neurospor
45	43.6	15.9	154561	8	AP002819	AP002819 Oryza sat

ALIGNMENTS

RESULT 1	AY066038	798 bp	mrna	linear	PLN 26-DEC-2001
LOCUS	Arabidopsis thaliana	At2g01290/F10A8.17	mrna, complete cds.		
DEFINITION	AY066038				
ACCESSION	AY066038.1	GI:17978866			
VERSION					
KEYWORDS	FLI CDNA.				
SOURCE	thale cress.				
ORGANISM	Arabidopsis thaliana				
REFERENCE	Kim,C.J., Chen,H., Cheuk,R., Meyers,M.C., Banh,J., Bowser,L., Carninci,P., Chang,E., Dale,J.M., Goldsmith,A.D., Hayshtizaki,Y., Ishida,J., Jones,T., Kamuya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Miranda,M., Natusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C., Toriumi,M., Wu,H.C., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.				
AUTHORS	Kim,C.J., Chen,H., Cheuk,R., Meyers,M.C., Banh,J., Bowser,L., Carninci,P., Chang,E., Dale,J.M., Goldsmith,A.D., Hayshtizaki,Y., Ishida,J., Jones,T., Kamuya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Miranda,M., Natusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C., Toriumi,M., Wu,H.C., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.				
TITLE	Arabidopsis ORF clones				
JOURNAL	Unpublished				

REFERENCE	2 (bases 1 to 98)
AUTHORS	Kim,C.J., Chen,H., Cheuk,R., Meyers,M.C., Banh,J., Bowser,L., Carninci,P., Chang,E., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C., Toriumi,M., Wu,H.C., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.
TITLE	Direct Submission
JOURNAL	Submitted (10-DEC-2001) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
COMMENT	Riken Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL CDNA : 'RIKEN Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K. The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Kim,C.J., Chen,H., Cheuk,R., Meyers,M.C., Shinn,P., Banh,J., Bowser,L., Chang,E., Dale,J.M., Goldsmith,A.D., Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Miranda,M., Nguyen,M., Onodera,C.S., Palm,C.J., Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Wu,H.C., Yamada,K., Yamamura, Y., Yu.G., Yu.S., Davis,R.W., Theologis,A., and Ecker,J.R. Kim,C.J. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk) contributed equally to this work as PIs. Location/Qualifiers 1..798 /organism="Arabidopsis thaliana" /db_xref="taxon:3702" /chromosome="2" /clone="U13949" /note="This clone is in pUNI 51 ecotype: Columbia" 1..798 /note="putative ribose 5-phosphate isomerase" /codon_start=1 /product="At2g01290/F10A8..17" /protein_id="AA147405.1" /db_xref="gi:17978867" /translation="MALADPLFTSDKSLAPDVAASPPQPNMLTDELAKRIAYKA VEPESGVLTIGSTAKAVHDPRIGELROGLTENIVETIPSKTOEALSLGIPLS DLDAPVILDSIGDAEDVPFINLVYRGSLIRKEMTGASKRKYVATVDKKMKHT GGSKIALPEVEIPIPCWKFPTAKRLSLLEGTCGANLRLEKGRAPVTIDGNITVDMAH EEDMDGAGSDAILRLPGVEHGMPFDNASTVIAGELGVKIKNH"
CDS	BASE COUNT ORIGIN 193 a 183 c 227 g 195 t
Query Match	29.7%: Score 81.4; DB 8; Length 798; Best Local Similarity 64.7%: Pred. No. 8.1e-06;
Matches 121:	Conservative 0; Mismatches 66; Indels 0; Gaps 0;
OY	88 accgccattcgcacccgagaagcgccgacggcccttcaccacctct 147 DB 17 ATCTCTCTCATTCATCGACAAATCTTTGCCCTTGATGTTCACGCC 76 OY 148 ccccctcgtcatctccaaccgaagcatttgaagaaatcgcgcgtacaagccgtcg 207 DB 77 CTCACCCATGAATTTAACAAGACAGACTCAAACTATCGCCGCTTACAAAAGCCTGC 136 OY 208 agtaagtgaagtcggcaatgtctcgtgacttagcgcgcgtccaccgccaagatgcgc 267 DB 137 AATTCGTGAGATCCGGCAGATGTCTCGGTCTCGAACCGGCTCACCGCAAACAGCGCG 196 OY 268 tcgacgcg 274
Db	197 TCGACGC 203
RESULT	2
AF360330	
LOCUS	AF360330 959 bp mRNA linear PLN 22-MAR-2001
DEFINITION	Arabidopsis thaliana putative ribose 5-phosphate isomerase (F23N20.9) mRNA, complete cds.
ACCESSION	AF360330.1 GI:13430835
VERSION	AF360330
SOURCE	FLJ_CDNA.
ORGANISM	thale cress. Arabidopsis thaliana
REFERENCE	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophytes: Magnoliophyta: eudicotyledons: core eudicots: Rosidae: eurosids II: Brassicales; Brassicaceae; Arabidopsi.
AUTHORS	1 (bases 1 to 959) Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A. Full length cDNA of gene F23N20.9 (GI:13232421) Unpublished 2 (bases 1 to 959) Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A. Direct Submission Submitted (14-MAR-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
COMMENT	RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL CDNA : 'RIKEN Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K. The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L., Lee,J.M., Quach,H.L., Toriumi,M., Yu.G., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A. Yamada,K. (SSP/PBEC) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PBEC) contributed equally to this work as PIs. Location/Qualifiers 1..959 /organism="Arabidopsis thaliana" /db_xref="taxon:3702" /chromosome="1" /clone="RAFLO9-14-P21 (R09450)" /note="This clone is in a modified pBluescript vector (pUC-1) as a BamHI/XhoI insert. ecotype: Columbia" 1..2 /gene="F23N20.9" /replac="compared to genomic sequence" /replace="fc" 1..26 /gene="F23N20.9" 1..959 /gene="F23N20.9" 27..830
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5' UTR	
gene	
CDS	

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/evidence=experimental
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/protein_id="AAK26040.1"
/db_xref="GI:13430836"
/translation="MGSAPDPLVATYEDLAAVNSAPPLSNLTQOEIKRTIAAYKAEV
ESGMVIGLGTSTAKHAAVARISLELRKGLNDIGIPSTTHEDQAVSIGPLSDIDS
HFWVDSIDGAEVDPALNLVKGSGSLREKMLIGASKRFVYIDESKLVYIGSG
LAPVEVVFCCDFTRKLEELFRDSCVAKLRMKIGSGEAAVAVDNRNVYVDLY
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misc_difference
747
/gene="P23N20.9"
/note="compared to genomic sequence resulting in an amino
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/replace="g"
831..959
3'UTR
/gene="P23N20.9"
BASE COUNT 254 a 188 c 265 g 252 t
ORIGIN
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Query Match 29.7%; Score 81.4; DB 8; Length 959;
Best Local Similarity 65.9%; Pred. No. 8e-06;
Matches 118; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Qy 96 ttcatcgccacgcagagaacgcgcacatgacgcgcctctccaccctctccctcc 155
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Db 39 TTGCATCCCTTGTCTGACGGCAGCTGAGATCTGCGCGCGTCAACTGCGCGCACATC 98

Qy 156 gtcatctcaccacaagacatttgaagaataatgcgcgcctacaaagccgtgagtcgt 215
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 99 TCAAACCTCAGCGAAGAACACTCAAGAAATCGCGCTTAAACCGCTGCAATTCGTC 158

Qy 216 gaatccgcgatgtgctcgcgcgcctgacgcgcgtccacgcgcacagatgcgcgcgacg 274
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 159 GAATCTGGAATGTTATCGCTCTCGGCACTGCTCCACCGCGAAGACCGCGTGCTCG 217

RESULT 3
AY054172 1464 bp mRNA linear PLN 30-SEP-2001
LOCUS Arabidopsis thaliana At2g01290/F10A8.17 mRNA, complete cds.
DEFINITION AY054172.1 GI:15809809
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 1464)
Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Banh,J.,
Bower,L., Carninci,P., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y.,
Ishida,J., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G.,
Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M.,
Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K.,
Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C.,
Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K.,
Davis,R.W., Theologis,A. and Ecker,J.R.
Arabidopsis cDNA clones
Unpublished
2 (bases 1 to 1464)
Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Banh,J.,
Bower,L., Carninci,P., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y.,
Ishida,J., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G.,
Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M.,
Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K.,
Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C.,
Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K.,
Davis,R.W., Theologis,A. and Ecker,J.R.
Direct Submission
Submitted (22-AUG-2001) Salk Institute Genomic Analysis Laboratory
JOURNAL (Signal), Plant Biology Laboratory, The Salk Institute for

Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL CDNAs (RAFL cDNA: 'RIKEN
Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J.,
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGSC (SSP) Consortium members carried out the
sequencing and annotation of the RAFL CDNAs: Cheuk,R., Chen,H.,
Kim,C.J., Koesema,E., Meyers,M.C., Shinn,P., Banh,J., Bower,L.,
Dale,J.M., Goldsmith,A.D., Jiang,P.X., Jones,T., Karlin-Neumann,G.,
Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M.,
Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Southwick,A.,
Tang,C.C., Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S.,
Davis,R.W., Theologis,A., and Ecker,J.R.

Cheuk,R. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to
this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)
contributed equally to this work as pIs.

Location/Qualifiers
1..1464
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/chromosome="2"
/clone="RAFL09-23-D14(R13949)"
/note="ecotype: Columbia"
1..393
394..1191
/note="putative ribose 5'-phosphate isomerase"
/codon_start=1
/product="At2g01290/F10A8.17"
/protein_id="AAU06833.1"
/db_xref="GI:15809810"
/translation="MALADPLFTSDKSLAFVYASPPQPMNLTODELRKIAVKA
VEFVSGMYLGLGTSTAKHAYDRIGELRLROGLKENVIGIPSKTQEDALSGLPLS
DIDAHVIDLSDGAEVDPFLNLVKGSGSLREKMLIGASKRFVYIDDSKRWKHI
GGSKLALPEVIFPCWKFPAEKLRLSLBEYGEANRLRGEKGAFTVDNRYIDMVH
EDMDGDLGAVSDAIIRLPGVEHGMFLMASVYIAGELGVKIKRKH"
1192..1464
3'UTR
BASE COUNT 325 a 336 c 320 g 483 t
ORIGIN

Query Match 29.7%; Score 81.4; DB 8; Length 1464;
Best Local Similarity 64.7%; Pred. No. 7.8e-06;
Matches 121; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy 88 accccattcatgccacgcagagaagccgcacatgacgcgcctctccaccctct 147
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Db 410 ATCCCTCTTTCATTAACATCGGACAAATCTTTCGCCCTTTGATGTGCTTTCACCGC 469

Qy 148 ccccccgcgcacatcccccacacagacatttgaagaataatgcgcgcctacaaagccgtg 207
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 470 CTGAGCCCATGAATTTAAACCAAGACGAGCTCAAGATATCGCCGCTTACAAAGCCGTGG 529

Qy 208 agtacgtgaatgcgcgcgtctcgcgcctagacacgcgcgtccacgcacaagcatgccg 267
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 530 AATTCTCGAGTCGCGCATGCTTCGTGCGGAACCGGCTCCACCGCAACACGCGG 589

Qy 268 tcgacgcg 274
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Db 590 TCGACCG 596

RESULT 4
AC016972 66653 bp DNA linear PLN 19-JAN-2001
LOCUS AC016972
DEFINITION Arabidopsis thaliana chromosome 1 BAC F23N20 genomic sequence,
complete sequence.
ACCESSION AC016972
VERSION AC016972.7 GI:12323418
KEYWORDS HTG.

LOCUS	A93589	1118 bp	DNA	Linear	PAT 22-JAN-2000
DEFINITION	Sequence 1 from Patent WO9737028.				
ACCESSION	A93589				
VERSION	A93589.1	GI:6741794			
KEYWORDS					
SOURCE	spinach.				
ORGANISM	Spinacia oleracea				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.				
AUTHORS	1 (bases 1 to 1118) Schnarrenberger C. and Leich J. EC 5.3.1.6)				
TITLE	RIBOSE-5-PHOSPHATE ISOMERASE (D-RIBOSE-5-PHOSPHATE KETOL ISOMERASE, Patent: WO 9737028-A 1 09-OCT-1997; SCHNARRENBERGER CLAUS (DE); BASF AG (DE)				
JOURNAL	Location/Qualifiers				
FEATURES	1..1118 /organism="Spinacia Oleracea"				
source	/db_xref="taxon:3562"				
5'UTR	15..24				
CDS	25..894 /note="unnamed protein product" /codon_start=1 /protein_id="CA869583.1" /db_xref="GI:6741795"				
3'UTR	/translation="MASAAFSLEPSTSTPPNRHATTKLNLKFLNHNRHKPFPTTTITLSLSPSPPTVLTQDDLLAKLAEEKAVSVSGMVLGLGTSTAFVAISRIGELLISACKRLTNIVGIPTSKRTEAQAASLGILPLSVLDHPRLIDLADIDAEVDPAVDNLVKRGALLREKVEAASDEFTIYVNDTKLYVDLGGSSRLAMPVEVOFCMKYMLKRIOLFKEKGCEAKLMEDSDSPRYTVDNSNYITVDLPFPIRSINDAAGAEISALBEVHEHGLEFLGNASEVTIIACKRTGVSYKTR"				
BASE COUNT	261 a	264 c	258 g	335 t	
ORIGIN	895..1118				
Query Match	24.8% Score 68; DB 6; Length 1118;				
Best Local Similarity	67.9%; Pred. No. 0.0024;				
Matches	95; Conservative 0; Mismatches 45; Indels 0; Gaps 0;				
Oy	135 ctcaacccttcctccctcgcgtcatccttcccgaagcgattgaaagaatcgccgc	194			
Db	163 CTCCTCTTCCTCCCTCCCACACACACTGTAACTCAAGACGATCTCAGAAGCTCGCCGC	222			
Oy	195 tacaaagcgcgcgaagtacgttagtgacggcatggtcccgagcgttagaccggtccacc	254			
Db	223 GAAAAAGCCGTCGACTCGCTCAATCGCGCATGTGTTCTCGGTCTCGGAACCGAAGTACT	282			
Oy	255 gccaaagcatgacgcgtcgaccg	274			
Db	283 GCCCGATTGCTGCTGCTCGCG	302			
RESULT 7					
SPIRSPIR	1118 bp mRNA linear PLN 13-FEB-2002				
LOCUS	Spinacia oleracea ribose-5-phosphate isomerase mRNA, complete cds;				
DEFINITION	nuclear gene for chloroplast product.				
ACCESSION	L43068				
VERSION	L43068.1	GI:18654316			
KEYWORDS	ribose 5-phosphate isomerase.				
SOURCE	spinach.				
ORGANISM	Spinacia oleracea				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.				
AUTHORS	1 (bases 1 to 1118) Matlin W., Henze K., Kellerman J., Flechner A. and Schnarrenberger C.				
TITLE	Microsequencing and cDNA cloning of the Calvin cycle/OOPP enzyme				
JOURNAL	ribiose-5-phosphate isomerase (EC 5.3.1.6) from spinach chloroplasts Plant Mol. Biol. 30 (4), 795-805 (1996)				

MEDLINE	96194461
FEATURES	
SOURCE	Location/Qualifiers 1..1118 /organism="Spinacia oleracea" /db_xref="taxon:3562"
5' UTR	1..24 /note="putative"
sig_peptide	25..174 /note="putative"
CDS	25..894 /EC.number="5.3.1.6" /note="cytosolic precursor of chloroplast protein putative"
	/codon_start=1 /product="ribosome-5-phosphate isomerase" /protein_id="AAL77389.1" /db_xref="GI:18654317"
	/translation="MASAAEFLPSTSTFNNRATYKLNLFHNRNKKPEFTTYTIIKSNSPIVLTPODDLKLAERKAVSDSVSGWVLGCGSTAFAVSRIQELLSACKLTVNGVPTSKRTAEQAASIGIPLSYVDHPRIDIALDGADVEDPDNLIVKRGEGALLREKNVEADSDFIYVDYDRLVDGLSGSRILAMPVEYVQPCWKYNLRQLQETFRKGCEAKLMGEDSSPYIVDINSNYIVDLTFPSINDAEAGREISALBSGVHEGLGNASEVI IAGKTGSVKTK"
	175..891 /note="5' end of mature subunit determined by protein sequencing putative"
	/product="ribosome-5-phosphate isomerase" 892..1118 /note="putative"
BASE COUNT	261 a 264 c 258 g 335 t
ORIGIN	
Query Match	24.8%; Score 68; DB 8; Length 1118;
Best Local Similarity	67.9%; Pred. No. 0.0024;
Matches 95; Conservative	0; Mismatches 45; Indels 0; Gaps 0;
Db	135 ctccaccccctcctccccctcgatcctcaaccacaagaagatttgaagaataatgcgccc 194 163 CTCCTTCCTCCCTCCCCAACACCAAGTCTTAATCATCAGATCTCAAGAAACTCGCCGCC 222
Db	195 tacaaagccgttcaggtaagtggatgcgatgtgcccgacttagagcacggcgtccacc 254 223 GAATAAAGCCGTGCATCGTCGTAACAATCCGGCATGGTTCTCGGTCGGAACCGGAAGTACT 282
Db	255 gccaaagcatgcctcgagaccg 274 283 GCCGCATTTCCTGCTGTCGCCG 302
RESULT 8	
AF154658	1084 bp mRNA linear PLN 15-JUN-2000
LOCUS	AF154658 Nicotiana tabacum clone P49 mRNA sequence.
DEFINITION	Nicotiana tabacum clone P49 mRNA sequence.
ACCESSION	AF154658
VERSION	AF154658.1 GI:8547158
KEYWORDS	
SOURCE	common tobacco.
ORGANISM	Nicotiana tabacum
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana. 1 (bases 1 to 1084) Sheehan,M.J., Wang,J. and Tinko,M.P. Characterization of cDNAs Differentially Expressed in Roots of Tobacco (Nicotiana tabacum cv Burley 21) During the Early Stages of Alkaloid Biosynthesis Unpublished 2 (bases 1 to 1084) Sheehan,M.J., Wang,J. and Tinko,M.P. Direct Submission Submitted (27-MAY-1999) Biology, University of Virginia, 044 Gilmer
JOURNAL	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	

FEATURES Hall, Charlottesville, Virginia 22903, USA
Location/Qualifiers

1. 1084

/organism="Nicotiana tabacum"

/cultivar="Burley 21"

/db_xref="taxon:4097"

/clone="PR49"

/issue_type="root"

/note="similar to ribose 5-phosphate isomerase"

BASE COUNT 286 a 245 c 250 g 302 t 1 others

Query Match

Best Local Similarity 78.7%; Score 62; DB 8; Length 1084;

Matches 74; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

OY 163 tcacccaagaagcattgagaagaatcgccgctacaaagcgtcgtgagtcgcg 222

DB 248 TAAACCAAGACGACACTCAAAAACCTGCGCGATTAACCGTCGTGAATACGTAAGACG 307

OY 223 gcatggtcctcgagcctagcaccggtccaccgc 256

DB 308 GAATGCTCCTGTGTAGCGACTGTTCAACCGC 341

RESULT 9

AP003944/C 135296 bp DNA linear HTG 26-JUL-2001

LOCUS Oryza sativa chromosome 6 clone OJ1126_F05, *** SEQUENCING IN

DEFINITION PROGRESS ***, in ordered pieces.

ACCESSION AP003944.1 GI:15021914

VERSION HTG; HTGS; PHASE2.

KEYWORDS Oryza sativa (cultivar:Nipponbare) DNA, clone:OJ1126_F05.

SOURCE Oryza sativa

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

AUTHORS Ehrhartoidae; Oryzeae; Oryza.

TITLE 1 (bases 1 to 135296)

JOURNAL Sasaki,T., Matsumoto,T. and Yamamoto,K.

REFERENCE Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, BAC

AUTHORS clone:OJ1126_F05

JOURNAL Published Only in Database (2001) In press

REFERENCE 2 (bases 1 to 135296)

AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.

JOURNAL Direct Submission

COMMENT Submitted (25-JUL-2001) Takuji Sasaki, National Institute of

Agrobiological Resources, Rice Genome Research Program; Kannondai

2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rpg.dna.affrc.go.jp/,

Tel:81-298-38-7441, Fax:81-298-38-7468)

The nucleotide sequence of this BAC clone was generated by

combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs

are represented as runs of N. The order of the pieces is believed

to be correct as given, however the sizes of the gaps between them

are based on estimates that have provided by the submitter. This

sequence will be replaced by the finished sequence as soon as it is

available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

FEATURES

source 1. 135296

/organism="Oryza sativa"

/cultivar="Nipponbare"

/db_xref="taxon:4530"

/chromosome="6"

/clone="OJ1126_F05"

BASE COUNT 39564 a 28425 c 29226 g 37721 t 360 others

Query Match 19.9%; Score 54.6; DB 2; Length 135296;

Best Local Similarity 54.8%; Pred. No. 0.54;

Matches 108; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

OY 61 ccttaacattaaatgcatccctaccacccattcatcgccaccgagaagccgca 120

DB 102410 CCTTCACGCGACGACGCGCTGCTACGACATCTCGCGCTTCGAGCGCCCA 102351

OY 121 tggacgcccgcctctccaccctccctccctccctccctccctccctccctcc 180

DB 102350 TCGCCGACGCGCTGCTACGCTCTCCGCTCCGCTCCGCTCCGCTCCGCTCC 102291

OY 181 agaaatcgccgctacaaagcgcgtcgaatcgtgagtcggcatgctcgcctag 240

DB 102290 AGGACGCGCATCGCATCGCGCCCTCCACGCCGTCMAAGCGGCGCATCACCCTGCTGCT 102231

OY 241 gcaccggtccaccgccc 257

DB 102230 CCGCCACGACACTTCGCG 102214

RESULT 10

AP004279 136775 bp DNA linear HTG 18-OCT-2001

LOCUS Oryza sativa chromosome 6 clone P0556B08, *** SEQUENCING IN

DEFINITION PROGRESS ***, in ordered pieces.

ACCESSION AP004279.1 GI:16215803

VERSION HTG; HTGS; PHASE2.

KEYWORDS Oryza sativa (cultivar:Nipponbare) DNA, clone:P0556B08.

SOURCE Oryza sativa

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

AUTHORS Ehrhartoidae; Oryzeae; Oryza.

TITLE 1 (bases 1 to 136775)

JOURNAL Sasaki,T., Matsumoto,T. and Yamamoto,K.

REFERENCE Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC

AUTHORS clone:P0556B08

JOURNAL Published Only in Database (2001) In press

REFERENCE 2 (bases 1 to 136775)

AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.

JOURNAL Direct Submission

COMMENT Submitted (17-OCT-2001) Takuji Sasaki, National Institute of

Agrobiological Sciences, Rice Genome Research Program; Kannondai

2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rpg.dna.affrc.go.jp/,

Tel:81-298-38-7441, Fax:81-298-38-7468)

NOTE: It currently consists of 1 contigs. Gaps between the contigs

are represented as runs of N. The order of the pieces is believed

to be correct as given, however the sizes of the pieces is believed

are based on estimates that have provided by the submitter. This

sequence will be replaced by the finished sequence as soon as it is

available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

FEATURES

source 1. 136775

/organism="Oryza sativa"

/cultivar="Nipponbare"

/db_xref="taxon:4530"

/chromosome="6"

/clone="P0556B08"

BASE COUNT 39254 a 29221 c 27596 g 40704 t

ORIGIN

Query Match 19.9%; Score 54.6; DB 2; Length 136775;

Best Local Similarity 54.8%; Pred. No. 0.54;

Matches 108; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

OY	61	ccttaacattaaatgagccattccctaccctccatcttccatgagccacgaagaagccggca	120
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OY	121	tggagccgagccgctctctccaccctctctccctcccgatcatcctcaaccaagacgattga	180
Db	117532	tcggcgcagcggtgacgctcattctccgctccgctccgagccgacccaacgactacgtcg	117591
OY	181	agaaatcgccgctcctaaagcgctgagtcgfggagtcggacatgctcgtgacctag	240
Db	117592	aggagccgactgcctcctccgcccctccctccacagccgctcctccgctcctc	117651
OY	241	gcaccgctccaccgccc	257
Db	117652	ccggcagcacttctggcc	117668
RESULT	11		
LOCUS	AP003616/c		
DEFINITION	AP003616	150638 bp	DNA
ACCESSION	Oryza sativa chromosome 6 clone P0490F09, *** SEQUENCING IN		
VERSION	AP003616		
KEYWORDS	AP003616.2 GI:15341241		
SOURCE	HTG: HTGS.PHASE2.		
ORGANISM	Oryza sativa (cultivar:Nipponbare) DNA, clone:P0490F09.		
REFERENCE	Oryza sativa		
AUTHORS	Euhayotop; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
TITLE	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
JOURNAL	Ehrhartoideae; Oryzeae; Oryza.		
REFERENCE	1 (bases 1 to 150638)		
AUTHORS	Sasaki,T., Matsumoto,T. and Yamamoto,K.		
TITLE	Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC		
JOURNAL	clone:P0490F09		
REFERENCE	2 (bases 1 to 150638)		
AUTHORS	Sasaki,T., Matsumoto,T. and Yamamoto,K.		
TITLE	Direct Submission		
JOURNAL	Submitted (10-MAY-2001) Takuji Sasaki, National Institute of		
REFERENCE	Agrobiological Resources, 305-8602, Japan		
AUTHORS	2-1-2, Tsukuba, Ibaraki 305-8602, Japan		
TITLE	(E-mail:tsasakigabr.aifrc.go.jp, URL:http://igp.dna.aifrc.go.jp/,		
JOURNAL	Tel:81-298-38-7441, Fax:81-298-38-7468)		
COMMENT	On Aug 28, 2001 this sequence version replaced gi:14020954.		
	NOTE: It currently consists of 1 contigs. Gaps between the contigs		
	are represented as runs of N. The order of the pieces is believed		
	to be correct as given, however the sizes of the gaps between them		
	are based on estimates that have provided by the submitter. This		
	sequence will be replaced by the finished sequence as soon as it is		
	available and the accession number will be preserved.		
	* NOTE: This is a 'working draft' sequence.		
	* This sequence will be replaced		
	* by the finished sequence as soon as it is available and		
	* the accession number will be preserved.		
FEATURES			
SOURCE	1. 150638		
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	/chromosome="6"		
	/clone="P0490F09"		
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ORIGIN			
OY	61	ccttaacattaaatgagccattccctaccctccatcttccatgagccacgaagaagccggca	120
Db	143219	ccttcaacagcagcagccgctgctacgctcctccgacatctctgcccctttcgagccggca	143160

FEATURES	SOURCE
LOCUS	AY045785
DEFINITION	Arabidopsis thaliana putative ribose 5-phosphate isomerase (F7018.28/At3g04790) mRNA, complete cds.
ACCESSION	AY045785
VERSION	AY045785.1 GI:15027856
KEYWORDS	FTL-CDNA.
ORGANISM	thale cress.
REFERENCE	Arabidopsis thaliana Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae, eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 998)
AUTHORS	Yamada, K., Liu, S.-X., Pham, P. K., Banh, J., Dale, J. M., Goldsmith, A. D., Jiang, P. X., Lee, J. M., Onodera, C. S., Quach, H. L., Tang, C. C., Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamlya, A., Kallin-Neumann, G., Kawai, J., Kim, C., Koeseema, E., Lam, B., Lin, J., Meyers, M. C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C. J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tracy, S. E., Shinozaki, K., Davis, R. W., Ecker, J. R. and Theologis, A.
TITLE	Full Length cDNA of gene F7018.28/At3g04790 (GI:15175179)
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 998)
AUTHORS	Yamada, K., Liu, S.-X., Pham, P. K., Banh, J., Dale, J. M., Goldsmith, A. D., Jiang, P. X., Lee, J. M., Onodera, C. S., Quach, H. L., Tang, C. C., Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamlya, A., Kallin-Neumann, G., Kawai, J., Kim, C., Koeseema, E., Lam, B., Lin, J., Meyers, M. C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C. J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tracy, S. E., Shinozaki, K., Davis, R. W., Ecker, J. R. and Theologis, A.
TITLE	Direct Submission
JOURNAL	Submitted (10-JUL-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
COMMENT	RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RFL cDNAs (RFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamlya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.
FEATURES	<p>The Salk, Stanford, PGSC (SSP) Consortium members carried out the sequencing and annotation of the RFL cDNAs: Yamada, K., Liu, S.-X., Pham, P. K., Banh, J., Dale, J. M., Goldsmith, A. D., Jiang, P. X., Lee, J. M., Onodera, C. S., Quach, H. L., Tang, C. C., Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Carninci, P., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Chen, H., Cheuk, R., Kallin-Neumann, G., Kim, C., Koeseema, E., Lam, B., Lin, J., Meyers, M. C., Miranda, M., Nguyen, M., Palm, C. J., Shinn, P., Southwick, A., Tracy, S. E., Davis, R. W., Ecker, J. R. and Theologis, A.</p> <p>Yamada, K. (SSP/PGSC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGSC) contributed equally to this work as PIs.</p> <p>Location/Qualifiers</p> <p>1..998</p> <p>/organism="Arabidopsis thaliana"</p> <p>/db_xref="taxon:3702"</p> <p>/chromosome="3"</p>

to

CDS
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9340..9386,9475..9669,9764..9810,9892..9958,10061..10161,
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11142..11489)
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NRMMSEFTALLIGTGVVILISRGKNSHLSESDDEFYLLPPIENMGFOVK
KQEPENFPTIARFALIGVIVVSCITISGAIQDFKIDIGFDGDLAIQAFPAADS
VCTIQVLMQDTEPLLILYSLVEGCVNATSVLPALQSDTLHLNHEAFQGNF
YLFELTSLGATGLISAVYIKTLTFRGSHSTDEVALMMIMATLSMLDEKLSLT
TFVFGIYMSHYVHWNVNESSRITKTHAFETLSFELEFELVQADALDIEMKRS
DSPGSAVASNLSLGMVLGMAFPAFVPLTSLCSLNKHOSEKISIQOQVIMWAGIR
GAVSALVANNFTFRSGHTELRGNALMTTSTIYCLSTWGMFKLPLRLYIMPHKA
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12957..>13082)
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the SAP protein (TR:E236624)) [Arabidopsis thaliana]"
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IYLFGEQVPLIDNNHHKFKMGILWYIHLLAGIYGMFPMYNSKMEERLPGVED
HSYRYPARPYKITYIMALNIGLSFACGLSLFGMLIGLITISVCYHAFLYPLL
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join(16215..16399,16873..16990,17073..17295,17473..17732)
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SLPTCSFVIRKA"
19191..19378

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CDS		/note="predicted by genefinder"
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		/db_xref="GI:1232853"
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gene		<22764..>26261
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		/protein_id="TA651418.1"
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TITLE
JOURNAL Arabidopsis thaliana chromosome III BAC F7018 genomic sequence
REFERENCE
2 (bases 1 to 95310)
AUTHORS Lin,X. and Kaul,S.
TITLE Direct Submission
JOURNAL Submitted (06-OCT-1999) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA, xlin@tigr.org
REFERENCE
3 (bases 1 to 95310)
AUTHORS Lin,X.
TITLE Direct Submission
JOURNAL Submitted (24-JAN-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
COMMENT On Jan 24, 2001 this sequence version replaced gi:12280830.
Address all correspondence to:
Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr.
Rockville, MD 20850, USA
e-mail: xlin@tigr.org
BAC clone F7018 is from Arabidopsis chromosome III and is near the
molecular marker ml172.
The orientation of the sequence is from SP6 to T7 end of the BAC
clone.

Genes were identified by a combination of three methods: Gene
prediction programs including GRAFT (available by anonymous ftp
from arthur.epm.ornl.gov), GeneFinder (Phil Green, University of
Washington), Genscan (Chris Burge,
http://genome.csf.stanford.edu/~chris/GENSCANW.html), and NetPlantene
(http://www.cds.dtu.dk/netgene/cbsnetgene.html), searches of the
EST database at TIGR (http://www.tigr.org/cdb/at/At.html).
Annotated genes are named to indicate the level of evidence for
their annotation. Genes with similarity to other proteins are named
after the database hits. Genes without significant peptide
similarity but with EST similarity are named as 'unknown' proteins.
Genes without protein or EST similarity, that are predicted by more
than two gene prediction programs over most of their length are
annotated as 'hypothetical' proteins. Genes encoding tRNAs are
predicted by tRNAscan-SF (Sean Eddy,
http://genome.wustl.edu/eddy/tRNAscan-SF/). Simple repeats are
identified by RepeatMasker (Brian Smrt,
http://ftp.genome.washington.edu/RM/RepeatMasker.html). Regions of
genomic sequence that are not annotated as genes but have predicted
exons by GRAFT are annotated as misc features.
Location/Qualifiers

FEATURES
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isoform 9) GB:AA03242 [Arabidopsis thaliana], similar to
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thaliana]; Pfam HMM hit: Eukaryotic protein kinase domain"
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WSAGVVIYMLAGEPFGNETAEDIFESTLRGNLPPPKKFSVSSEAKDLKRWIC
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repeat_region

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complement(1965..2063)
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GDCLSEIYVROSREKNKNSDQRTSMLDALGVASEKAKNLTNLELGDKEAEKEX
KKREEVAKIRLPVVRKLFGEVAETSVVYLPVCKAEGERKILEAEMETIAGDFV
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DRSRAVYALHLESAQDVAVCELDKRSQNLITITFAVAVANDLFTGDSNPFKTRIRI
KEASIDLPVTEEDVDVAALAEAAVKDGDGOTQOVAAEASAGDNVAVSDPRL
DAWIPSSGKNGKTKIKRTNEDDAENKRFSLKREALITLCTEIAARYKPKQCTV
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mRNA

Query Match 19.7%; Score 54; DB:8; Length 95310;
Best Local Similarity 52.7%; Pred. No. 0.72;
Matches 117; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

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DB 91734 TCGTTCTCTCTTCACCTTACCTACGCACTCCTTATGCGCTACGACACTGGCT 91793
|||||

QY 112 aagcgccatgagcgagcgagcctctccacccctctccctccgctcatctcaaccaag 171
|||||
DB 91794 CTCTCTCGAACCCTCGCTTCACTTCGCGCAAGGCTCAATCGCTTCGCTTACACAG 91853
|||||

QY 172 acgattgaagaataatgcgcgctacaaagccgtcgagtaagtgagtcgagcatgtcc 231
|||||
DB 91854 ACGATTGGAAGAGACTGCGCGGAGAAAGCTGTGGAGGCAATTAACCTGGATGGTTC 91913
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QY 232 tcggcctlaagcaccgctcaccgacgcaagcatgcgcgtcagacc 273
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DB 91914 TAGGGCTCGAACCAGCAACCGCACTTCGCTGTGATC 91955
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RESULT 15
AX172623
LOCUS AX172623 454 bp DNA Linear PAT 03-JUL-2001
DEFINITION Sequence 113 from Patent WO0144476.
ACCESSION AX172623
VERSION AX172623.1 GI:14597735
KEYWORDS
SOURCE Physcomitrella patens.
ORGANISM Physcomitrella patens
Bryophyta: Viridiplantae: Streptophyta: Embryophyta: Bryophyta:
Bryopsida: Funariidae: Funariales: Funariaceae: Physcomitrella.
REFERENCE 1 (bases 1 to 454)

AUTHORS Lerchl,J., Renz,A., Ehrhardt,T., Reindl,A., Cirpus,P., Bischoff,F.,
Frank,M., Freund,A., Duwenig,E., Schmidt,R.M. and Reski,R.
TITLE Moss genes from Physcomitrella patens encoding proteins involved in
the synthesis of carbohydrates
JOURNAL Patent: WO 0144476-A 113 21-JUN-2001;
BASF Plant Science GmbH (DE)
FEATURES
source Location/Qualifiers
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BASE COUNT 96 a 115 c 135 g 101 t 7 others
ORIGIN

Query Match 18.0%; Score 49.2; DB:6; Length 454;
Best Local Similarity 57.2%; Pred. No. 7.8;
Matches 87; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

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DB 235 CACGATGGCTTCCGTCGCCGCAATCCGCAAGCTTACACAGATGAAC 294
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QY 179 gaagaaatgcgcgctcacaagcgctcgagtgagtcgagcgcgagtcctccgacct 238
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DB 295 CAAAGAGTTGCTCCCNAGAGGCTGTGGAAATATGCAAGAGTGGCATTGGGTT 354
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QY 239 aggcacggtccacgcgcgcaagcatgcgctcg 270
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DB 355 GGGCACAAGTTCTTACAGCTGATTTGCAGTGG 386
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Job time: 49006 sec

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OM nucleic - nucleic search, using sw model

Run on: July 3, 2002, 03:38:57 ; Search time 6582.52 Seconds

(without alignments)
561.816 Million cell updates/sec

Title: US-09-300-482-311

Sequence: 1 ctacattcttctccacc.....gccaaagcatgcgcgcgacgcg 274

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlma:*
5: em_estlov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_estc2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vtl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	189.6	69.2	569	10	BM093169 saj05h04.
2	141.6	51.7	411	9	AV412358 AV412358
3	133.6	48.8	520	10	BF645504 NF034G05E
4	133.6	48.8	562	10	BF520202 EST457671
5	133.6	48.8	563	9	AM559864 EST314912
6	133.6	48.8	668	9	AM559587 EST314635
7	133.6	48.8	679	10	BG647838 EST509457
8	133.6	48.8	704	10	BG584469 EST486229
9	133.6	48.8	808	10	BG582993 EST484732
10	126.4	46.1	428	9	AI900328 sc04b07.y
11	112	40.9	275	9	AV424584 AV424584
12	107.2	39.1	722	10	BG585240 EST487003
13	102.8	37.5	636	10	BI309133 EST530543
14	99	36.1	265	9	AV412159 AV412159
15	96.8	35.3	745	12	AV412011 AV412011
16	94.2	34.4	457	10	BH600444 BGCND38TF
17					BI139102 FI23P33Y

18	88	32.1	309	9	AV416699	AV416699
19	88	32.1	366	9	AV420477	AV420477
20	88	32.1	374	9	AV414597	AV414597
21	88	32.1	379	9	AV421081	AV421081
22	88	32.1	382	9	AV415702	AV415702
23	88	32.1	385	9	AV424000	AV424000
24	88	32.1	389	9	AV407718	AV407718
25	88	32.1	395	9	AV413372	AV413372
26	88	32.1	405	9	AV422025	AV422025
27	88	32.1	422	9	AV425897	AV425897
28	88	32.1	425	9	AV426595	AV426595
29	88	32.1	426	9	AV407869	AV407869
30	88	32.1	428	9	AV418494	AV418494
31	88	32.1	429	9	AV411127	AV411127
32	88	32.1	466	10	BI417490	BI417490
33	88	32.1	471	9	AV422350	AV422350
34	88	32.1	554	10	BI420175	BI420175
35	88	32.1	571	10	BI418851	BI418851
36	88	32.1	573	9	AM720035	AM720035
37	87.6	32.0	481	10	BF067532	BF067532
38	87.6	32.0	501	10	BI498790	BI498790
39	87.6	32.0	502	10	BG363532	BG363532
40	87.6	32.0	595	10	BF067604	BF067604
41	87.6	32.0	604	10	BG042907	BG042907
42	87.6	32.0	611	9	BE191266	BE191266
43	86.6	31.6	322	9	AV428885	AV428885
44	86	31.4	368	9	AI460598	AI460598
45	86	31.4	395	10	BE609370	BE609370

ALIGNMENTS

RESULT 1
LOCUS BM093169
DEFINITION saj05h04.y1 Gm-cl065 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-cl065-9584.5' similar to SW:RPLA_ARATH_O92U03 PROBABLE
RIBOSE 5-PHOSPHATE ISOMERASE ; mRNA sequence.

ACCESSION BM093169
VERSION BM093169.1
KEYWORDS GI:17022135
SOURCE EST.

ORGANISM soybean.
Glycine max

REFERENCE 1 (bases 1 to 569)
Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna
'A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
'Y., Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurk
'R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
'R., Waterston,R. and Wilson,R.
Public Soybean EST Project

TITLE JOURNAL
COMMENT Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

FEATURES
source
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 421.
Location/Qualifiers
1..569
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl065-9584"

with *Phytophthora medicaginis*"

BASE COUNT	140 a	193 c	72 g	158 t
ORIGIN				
Query Match		48.8%	Score 133.6;	DB 9; Length 563;
Best Local Similarity		80.8%;	Pred. No. 1.5e-17;	
Matches 173; Conservative		0;	Mismatches 29;	Indels 12; Gaps 1
QY 73	acatggcattccctacccatcttcatgcccacgaagaagccgcatggagccgc	132		
DB 226	AGATGGCATTCCTTTCGCCCCCATTTATCTTCCTCCGCAAAAGCGGCATGAAACCGGCTC	285		
QY 133	tctctcaacccctctctccc-----cttcgtlcatctcaaccagaacgatttga	180		
DB 286	TCTCTCATCCCTTCCTCCCATCTTCCTCCGCTCCGTCATCCATCCCAAGACGATTTGA	345		
QY 181	agaanaatcgccgcctcaagaagccgtgagtagtggagcgcgcgaatggctcgactcg	240		
DB 346	AGAAATATCGCCGCGCTCAAAAGCGCGTGAATAGCTCAATTCGGTATGGTTAGCGCTCG	405		
QY 241	gacccggctccacacgcgaacgcatgcgcgtgacgcg	274		
DB 406	GAACCGCTTCAACCGCCAAACAGCGCTGCGCCG	439		
RESULT 6				
AM559587		668 bp	mRNA	linear EST 07-SEP-2000
LOCUS	EST114635 DSIR Medicago truncatula cDNA clone PDSIR-24115, mRNA			
DEFINITION	sequence.			
ACCESSION	AM559587			
VERSION	AM559587.1			
KEYWORDS	GI:7205013			
SOURCE	EST.			
ORGANISM	barrel medic.			
	Medicago truncatula			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
	Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;			
	Medicago.			
REFERENCE	1 (bases 1 to 668)			
AUTHORS	Fedorova,M., Plerson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Peng			
	H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S.,			
	Holt,I.E. and Fraser,C.M.			
	ESTs from roots of Medicago truncatula after inoculation with			
	Phytophthora medicaginis			
	Unpublished (1999)			
JOURNAL	Contact: Carroll P. Vance			
COMMENT	Department of Agronomy and Plant Genetics			
	University of Minnesota			
	411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA			
	Tel: 612 625 5715			
	Fax: 651-649-5058			
	Email: Vance004@maroon.tc.umn.edu			
	Minnesota EST name:M250873e ; TIGR sequence name:MTBAM56TK ; More			
	information, including clone ordering, is available at: .			
	'http://chryslie.tamu.edu/medicago'			
	Seq primer: SKmod (CTA gAA CTA gTg gAT CC).			
	location/Qualifiers			
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	/cultivar="genotype A17"			
	/db_xref="taxon:3880"			

[illegible]

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/cultivar="A17"
/db_xref="taxon:3880"
/clone="pHOGA-18E7"
/clone_1ib="HOGA"
/rustse_type="3 day old seedling roots"
/dev_stage="24 hours after treatment in the dark at 26 C
with 0.5 mg/ml oligogalacturonides (DP 6-20) in the
presence of 100 ug/ml Gentamicin"
/lab_host="X10LR"
/note="Vector: pbluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-zap phage using Ex-assist
helper phage and propagated in SOLR cells."
BASE COUNT
167 a 216 c 104 g 192 t
ORIGIN

```

Query Match	48.8%;	Score 133.6;	DB 10;	Length 679;
Best Local Similarity	80.8%;	Pred. No. 1.6e-17;		
Matches 173; Conservative	0;	Mismatches 29;	Indels 12;	Gaps 1;

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library"
/cultivar="Medicago truncatula genotype A17"
/db_xref="taxon:119092"
/clone="pMAM-15N9"
/clone_lib="MAM"
/tissue_type="Roots colonized with Glomus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host="E. coli strain XOLR"
/vector="Vector: pluescript SK-; Site.1: EcoRI; Site.2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The cDNA was
directionally ligated into the unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-zap phage using Ex-assist
helper phage and propagated in XOLR cells."

```

BASE COUNT	176 a	196 c	124 g	208 t
ORIGIN				

Query Match	48.8%;	Score 133.6;	DB 10;	Length 704;
Best Local Similarity	80.8%;	Pred. No. 1.6e-17;		
Matches 173; Conservative	0;	Mismatches 29;	Indels 12;	Gaps 1,

RESULT	8
BG584469	
LOCUS	704 bp
DEFINITION	MMAM Medicago truncatula/Gliomus versiforme mixed EST
DESCRIPTION	library CDNA clone pmHAM-15N9 5' end, mRNA sequence.
ACCESSION	U00944.0

FEATURES	Location/Qualifiers
source	1..704
	/Organism="Medicago truncatula/silomus versiforme mixed EST

RESULT	9
BG582993	
LOCUS	808 bp mRNA linear EST 11-Apr-2001
DEFINITION	BG582993
ACCESSION	EST486732 GVN Medicago truncatula cDNA clone pCVN-71E12 5' end,
VERSION	mRNA sequence.
KEYWORDS	BG582993 BG582993.1 GI:13598049
SOURCE	EST.
ORGANISM	barrel medic. Medicago truncatula Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons, core eudicots, Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Trifolioideae; Medicago.
REFERENCE	1 (bases 1 to 808)
AUTHORS	Fedorova,M., Plerson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Town C.D., Van Aken,S., Utecherack,T., Cho,Y. and Fraser,C.M.
TITLE	ESTs from one month old nitrogen-fixing root nodules of Medicago truncatula, 2001
JOURNAL	unpublished (2001)
COMMENT	Contact: Carroll P. Vance

/clone="pGPOD-10D22"
/clone_lib="GPOD"
/tissue_type="Immature pod walls"
/dev_stage="Immature pods, ranging in age from 15 to 30 days after pollination"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Immature pods, ranging in age from 15 to 30 days after pollination, were collected from greenhouse-grown plants. At harvest, seeds were removed from pods and isolated pod walls were collected and immediately frozen in liquid nitrogen. Pod walls were pooled for mRNA extraction. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XL0LR cells."

BASE COUNT 157 a 135 c 149 g 195 t

ORIGIN

Query Match 37.5%; Score 102.8; DB 10; Length 636;
Best Local Similarity 84.1%; Pred. No. 2.5e-11;
Matches 116; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

OY 137 caaccctctccctccctccgtcgtcctccacccaagcagattgaagaaatcgccgcta 196
DB 24 cccattctctccgtccgtccgtatccctatccacagacattgagaaatcgccgcta 83

OY 197 caaggccgctgagtagtgagtcgagcagtcgtctcgcagcagccagcgtccacgc 256
DB 84 CAAAGCCGTCGAATACGTGATCCGGATGCTTACAGCCTCGAACCAGGTTCAACCGC 143

OY 257 caagcatgcgtcgacgcg 274
DB 144 CAACACGCGCGTCGCCG 161

RESULT 14
AV412159 265 bp mRNA linear EST 23-MAY-2000
LOCUS AV412159 Lotus japonicus young plants (two-week old) Lotus
DEFINITION AV412159 Lotus japonicus young plants (two-week old) Lotus
ACCESSION AV412159
VERSION AV412159.1 GI:7741323
KEYWORDS EST.
SOURCE Lotus japonicus.
ORGANISM Lotus japonicus.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae;
Lotus.
1 (bases 1 to 265)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
Generation of 7137 non-redundant expressed sequence tags from a
legume, Lotus japonicus
DNA Res. 7 (2), 127-130 (2000)
JOURNAL MEDLINE
COMMENT Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakam@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/
location/Qualifiers
1. 265
/organism="Lotus japonicus"
/db_xref="taxon:34305"
/clone_lib="MM2161f10_r"
/dev_stage="young plants (two-week old)"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; isolate=Miyakojima MG-20"

FEATURES
source

BASE COUNT

54 a 92 c 31 g 88 t

ORIGIN

Query Match 36.1%; Score 99; DB 9; Length 265;
Best Local Similarity 78.7%; Pred. No. 1.3e-10;
Matches 133; Conservative 0; Mismatches 30; Indels 6; Gaps 1;

OY 57 tcaaccttaacatnaacatgccaatccctaccacattcatcgccagagaagcc 116
DB 103 TCTCTCTCGATTTCATATGCTATTCCTATCCCATTTTCATCTCTCCGAAAGCA 162

OY 117 gccatgagcgcgcctccctccaccctccctccctccctccctccctccctccctcc 176
DB 163 GCCATGAGACAGAGGCTTCTCGACCAT-----CCTCCATCATCTTCACCAAGAGAT 216

OY 177 ttgaagaaatcgccgcctacaagcgcgtgagtagctggagtcgcgca 225
DB 217 TTGAAGAAATCGCCGCTTACAAAGCCGTGAGTATCGAATCCGGCA 265

RESULT 15
AV412011 266 bp mRNA linear EST 23-MAY-2000
LOCUS AV412011 Lotus japonicus young plants (two-week old) Lotus
DEFINITION AV412011 Lotus japonicus young plants (two-week old) Lotus
ACCESSION AV412011
VERSION AV412011.1 GI:7741175
KEYWORDS EST.
SOURCE Lotus japonicus.
ORGANISM Lotus japonicus.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae;
Lotus.
1 (bases 1 to 266)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
Generation of 7137 non-redundant expressed sequence tags from a
legume, Lotus japonicus
DNA Res. 7 (2), 127-130 (2000)
JOURNAL MEDLINE
COMMENT Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakam@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/
location/Qualifiers
1. 266
/organism="Lotus japonicus"
/db_xref="taxon:34305"
/clone_lib="MM214a02_r"
/dev_stage="young plants (two-week old)"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; isolate=Miyakojima MG-20"

BASE COUNT 54 a 94 c 30 g 88 t

ORIGIN

Query Match 36.1%; Score 99; DB 9; Length 266;
Best Local Similarity 78.7%; Pred. No. 1.3e-10;
Matches 133; Conservative 0; Mismatches 30; Indels 6; Gaps 1;

OY 57 tcaaccttaacatnaacatgccaatccctaccacattcatcgccagagaagcc 116
DB 104 TCTCTCTCGATTTCATATGCTATTCCTATCCCATTTTCATCTCTCCGAAAGCA 163

OY 117 gccatgagcgcgcctccctccaccctccctccctccctccctccctccctccctcc 176
DB 164 GCCATGAGACAGAGGCTTCTCGACCAT-----CCTCCATCATCTTCACCAAGAGAT 217

OY 177 ttgaagaaatcgccgcctacaagcgcgtgagtagctggagtcgcgca 225
DB 218 TTGAAGAAATCGCCGCTTACAAAGCCGTGAGTATCGAATCCGGCA 266

Wed Jul 3 12:01:15 2002

us-09-300-482-311.rst

Page 9

Search completed: July 3, 2002, 03:39:00
Job time: 43320 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 3, 2002, 07:57:43 ; Search time 796.36 Seconds

(without alignments)
590.731 Million cell updates/sec

Title: US-09-300-482-311

Perfect score: 274
1 ctaccatccttcctccacc.....gccaaagatgcgcgtcaccg 274

Sequence:

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	81.4	29.7	942	21	AAC37420	Arabidopsis thaliana
2	81.4	29.7	1429	21	AAC47590	Arabidopsis thaliana
3	81.4	29.7	1569	21	AAC47074	Arabidopsis thaliana
4	68	24.8	1118	18	AAR87859	DNA encoding ribos
5	54	19.7	966	21	AAC45894	Arabidopsis thaliana
6	54	19.7	967	21	AAA78440	Plant SDF polynuc
7	49.2	18.0	454	22	AAH88764	Ribose-5-Page-ism
8	44.6	16.3	77536	21	AAH14651	Nucleotide sequenc
9	43.4	15.8	1233	22	AAH44089	Oryza sativa perox

10	43	15.7	701	18	AA94500	GAL4 DNA binding d
11	43	15.7	38734	20	AA32020	Human MERT1 relate
12	43	15.7	38734	22	AAC90077	AL021529 cDNA clon
13	42.6	15.5	1371	21	AA287214	DNA encoding synth
14	42.6	15.5	1371	22	AA54486	Botulin toxin hea
15	42	15.3	771	20	AA12317	Neisseria meningit
16	41.8	15.3	833	15	AA064203	snab gene encoding
17	41.8	15.3	882	19	AA064512	M. tuberculosis im
18	41.8	15.3	882	19	AAV44403	Mycobacterium tube
19	41.8	15.3	882	20	AA219313	M. tuberculosis an
20	41.8	15.3	882	20	AA219101	M. tuberculosis re
21	41.8	15.3	5392	15	AA064201	Sequence compisrin
22	41.8	15.3	4411529	22	AA199682	Mycobacterium tube
23	41.6	15.2	230	18	AA191500	Mycobacterium tube
24	41.6	15.2	290	18	AA191436	Mycobacterium tube
25	41.6	15.2	290	19	AAV64483	M. tuberculosis im
26	41.6	15.2	290	19	AAV44375	Mycobacterium tube
27	41.6	15.2	290	20	AA219285	M. tuberculosis an
28	41.6	15.2	290	20	AA219073	M. tuberculosis re
29	41.6	15.2	1929	19	AAV57472	Sorghum bicolor (L
30	41.4	15.1	490	21	AAV79485	Eucahyptus grandis
31	41.4	15.1	4403765	22	AA199683	Mycobacterium tube
32	41	15.0	3632	17	AA106978	T. thermophilus ga
33	41	15.0	3632	20	AA21373	Thermus thermophil
34	41	15.0	3849	22	AA25795	S. chrysomallus ac
35	40.8	14.9	985	19	AAV64548	M. tuberculosis im
36	40.8	14.9	985	19	AAV44439	Mycobacterium tube
37	40.8	14.9	985	20	AA219349	M. tuberculosis an
38	40.8	14.9	985	20	AA219137	M. tuberculosis re
39	40.8	14.9	27541	22	AA17185	Streptomyces nous
40	40.8	14.9	125401	22	AA17186	Streptomyces nous
41	40.4	14.7	1236	16	AA745060	Waite T52 cDNA nuc
42	40.4	14.7	1248	21	AA287286	S. venezuelae deso
43	40.4	14.7	1600	22	AA44793	Cysteine protease
44	40.4	14.7	5970	21	AAV75635	Nucleotide sequenc
45	40.4	14.7	5970	21	AA256003	Contig 002 from co

ALIGNMENTS

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RESULT 1
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ID AAC37420 standard; DNA; 942 BP.
XX
AC AAC37420:
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 17312.
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DB 508 atccctcttattacatcgacaatcttgcgccttgatgtgccttcacgc 567
   ||| ||||| ||| ||||| ||| ||| ||| ||| ||| |||
QY 148 cccctcgtatcctcaccacagagattgaagaatcgcgcctacagcgctcg 207
   ||| ||||| ||| ||||| ||| ||| ||| ||| ||| |||
DB 568 ctcaagccatgaatttaacacagacagatcaacgctacgcgttacaaagcgctg 627
   ||| ||||| ||| ||||| ||| ||| ||| ||| ||| |||
QY 208 agtacgtgaagtcgcgcgttcctcgcctcagacgcgcgttcacgcgcagatgcg 267
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 628 aatcgctgaagtcgcgcgttctcgtctcgcgaaccgcgtccacgcgcacacgcg 687
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 268 tcgacgcg 274
   ||||| |||||
DB 688 tcgacgcg 694

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RESULT 4
AAT87859
ID AAT87859 standard; cDNA; 1118 BP.
AC AAT87859;
XX
DT 21-APR-1998 (first entry)
XX
DE DNA encoding ribose-5-phosphate isomerase.
XX
KW Ribose-5-phosphate isomerase; screen; inhibitor; herbicidal agent;
KM ss.
XX
OS Spinacia oleracea.
XX
FH Key Location/Qualifiers
FT CDS 25..894
FT /*tag= a
FT /product= ribose-5-phosphate_isomerase
XX
PN W09737028-A2.

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XX 09-OCT-1997.
PD
XX 26-MAR-1997; 97WO-EP01539.
EF
XX 29-MAR-1996; 96DE-4012772.
PR
XX (BADI ) BASF AG.
XX
XX Kellermann J, Lerchl J, Schmidt R, Schnarrenberger C;
PI William M;
XX WPI: 1997-503113/46.
DR P-PDSB: AAM27505.
XX
XX Spinach ribose-5-phosphate isomerase - useful to screen for
PT inhibitors, i.e. herbicidal agents
XX
XX Claim 5; Figure 2; 22pp; German.
PS
XX The present sequence represents DNA encoding a novel spinach ribose-5-
CC phosphate isomerase. The invention relates to a protein with ribose-5-
CC phosphate isomerase activity, comprising at least 100 residues of a 289
CC residue spinach amino sequence, preferably residues 50-239. Novel
CC phosphate isomerase inhibitors can be identified by incubating potential
CC inhibitors with the enzyme and determining the ribose-5-phosphate
CC isomerase activity. These inhibitors can be used as herbicidal agents.
XX
SQ Sequence 1118 BP; 261 A; 264 C; 258 G; 335 T; 0 other;

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Query Match 24.8%; Score 68; DB 18; Length 1118;
 Best Local Similarity 67.9%; Pred. No. 7.9e-08;

Matches 95; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

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QY 135 ctccaccctcctccctcgcgtatcctcaccacagacgattgaagaatcgcgcgc 194
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DB 163 ctctctctcctccccaacacagctcttaactcaagacgatcagaactcgcgcgc 222
   ||| ||||| ||| ||||| ||| ||| ||| ||| ||| |||
QY 195 tacaagcgcgtgaagtcgagtcgcgcgttcctcgcctcgaagcgcgcctcacc 254
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DB 223 gaagaagcgcgtcgcacacgaatccgcatgtctcgtctcgaacgcgaagtact 282
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QY 255 gcccaagatgcgcgtcgacgcg 274
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DB 283 gccgcattgtgtctcgcgcg 302

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RESULT 5
AAC45894
ID AAC45894 standard; DNA; 966 BP.
XX
AC AAC45894;
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DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 48154.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.

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PR 23-MAR-1999; 9905-0125788.
PR 23-MAR-1999; 9905-0126264.
PR 29-MAR-1999; 9905-0126785.
PR 01-APR-1999; 9905-0127462.
PR 06-APR-1999; 9905-0128234.
PR 08-APR-1999; 9905-0128714.
PR 16-APR-1999; 9905-0129845.
PR 19-APR-1999; 9905-0130077.
PR 21-APR-1999; 9905-0130449.
PR 23-APR-1999; 9905-0130510.
PR 28-APR-1999; 9905-0130891.
PR 30-APR-1999; 9905-0131449.
PR 30-APR-1999; 9905-0132048.
PR 04-MAY-1999; 9905-0132407.
PR 05-MAY-1999; 9905-0132485.
PR 06-MAY-1999; 9905-0132486.
PR 07-MAY-1999; 9905-0132487.
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PR 14-MAY-1999; 9905-0134221.
PR 18-MAY-1999; 9905-0134370.
PR 18-MAY-1999; 9905-0134768.
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PR 20-MAY-1999; 9905-0135124.
PR 21-MAY-1999; 9905-0135353.
PR 24-MAY-1999; 9905-0135629.
PR 25-MAY-1999; 9905-0136021.
PR 27-MAY-1999; 9905-0136392.
PR 28-MAY-1999; 9905-0136782.
PR 01-JUN-1999; 9905-0137222.
PR 03-JUN-1999; 9905-0137528.
PR 04-JUN-1999; 9905-0137502.
PR 07-JUN-1999; 9905-0137724.
PR 08-JUN-1999; 9905-0138094.
PR 10-JUN-1999; 9905-0138540.
PR 14-JUN-1999; 9905-0139119.
PR 16-JUN-1999; 9905-0139452.
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PR 17-JUN-1999; 9905-0139492.
PR 18-JUN-1999; 9905-0139454.
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PR 18-JUN-1999; 9905-0139750.
PR 18-JUN-1999; 9905-0139763.
PR 21-JUN-1999; 9905-0139817.
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PR 24-JUN-1999; 9905-0140354.
PR 24-JUN-1999; 9905-0140695.
PR 28-JUN-1999; 9905-0140823.
PR 29-JUN-1999; 9905-0140931.
PR 30-JUN-1999; 9905-0141287.
PR 01-JUL-1999; 9905-0141842.
PR 01-JUL-1999; 9905-0142154.
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PR 22-JUL-1999; 9905-0145089.
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PR 23-AUG-1999; 9905-0149902.
PR 23-AUG-1999; 9905-0149930.
PR 25-AUG-1999; 9905-0150566.
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PR 27-AUG-1999; 9905-0151065.
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PR 27-AUG-1999; 9905-0151080.
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PR 31-AUG-1999; 9905-0151438.
PR 01-SEP-1999; 9905-0151930.
PR 07-SEP-1999; 9905-0152363.
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PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Matches 117; Conservative 0; Mismatches 105; Indels 0; Gaps 0;
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QY 112 aagcgacatgagcgccgctccctccacccctctccctccgttcattcaccacaag 171
DB 118 ctctctctcgaaacctccgtttcatcttcgttaaggtcaatccgttcgcttccacagg 177
QY 172 acgatttgaagaataatcgccgcttacaagcgctcgagtaagtcgagcggacatgagcc 231
DB 178 acgatttgaagaagctcgcgagcggaagctgtgaggaatataaccttggatgtctc 237
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DB 238 tagggctcggaacggacgacccagcagcttgcgtgtgaccc 279
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RESULT 6
AAA78440
ID AAA78440 standard; DNA; 967 BP.
AC AAA78440;
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DT 27-NOV-2000 (first entry)
XX Plant SDF polynucleotide sequence SEQ List 1 NO:25.
DE Plant SDF polynucleotide sequence SEQ List 1 NO:25.
KW Plant: corn; Arabidopsis thaliana; sequence-determined DNA fragment;
KW SDF: genetic mapping; identification; promoter; structural gene; UTR;
KW untranslated region; expression control; ds.
XX Plant.
OS Plant.
XX WO2000040695-A2.
XX 13-JUL-2000.
XX
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PF 07-JAN-2000; 2000MO-US00466.
XX 08-JAN-1999; 99US-0115293.
PR (CERE-) CERES INC.
PA Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L;
PI WPI, 2000-465970/40.
XX
PT New corn plant and Arabidopsis thaliana sequence-determined DNA
PT fragments, useful for expressing gene products and for controlling
PT expression of a target gene -
XX
XX Claim 1: Page 337; 673pp; English.
PS
CC The present invention describes polynucleotides, such as complete cDNA
CC sequences and/or sequences of genomic DNA encompassing complete genes,
CC portions of genes, and/or intergenic regions, collectively referred to
CC as sequence-determined DNA fragments (SDFs), from corn plants and
CC Arabidopsis thaliana. The SDFs are promoters, structural genes,
CC untranslated regions (UTRs), or 3' termination sequences. They can be
CC used for expressing a gene product and controlling expression of a
CC target gene, either as a promoter, a structural gene, an UTR or as a
CC 3' termination sequence. They are also useful as tools for genetic
CC mapping, and identification of a particular individual plant or for
CC clustering a group of plants with a common trait. AAA78433 to AAA78630
CC and AAB24605 to AAB25099 represent the specifically claimed
CC polynucleotide sequences and polypeptides encoded by them given in the
CC present invention.
XX
SQ Sequence 967 BP; 232 A; 201 C; 229 G; 305 T; 0 other;
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Query Match 19.7%; Score 54; DB 21; Length 967;
Best Local Similarity 52.7%; Pred. No. 0.00024;
Matches 117; Conservative 0; Mismatches 105; Indels 0; Gaps 0;
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QY 112 aagcgacatgagcgccgctccctccacccctctccctccgttcattcaccacaag 171
DB 118 ctctctctcgaaacctccgtttcatcttcgttaaggtcaatccgttcgcttccacagg 177
QY 172 acgatttgaagaataatcgccgcttacaagcgctcgagtaagtcgagcggacatgagcc 231
DB 178 acgatttgaagaagctcgcgagcggaagctgtgaggaatataaccttggatgtctc 237
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DB 238 tagggctcggaacggacgacccagcagcttgcgtgtgaccc 279
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RESULT 7
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ID AAH8764 standard; CDNA; 454 BP.
AC AAH8764;
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DT 28-SEP-2001 (first entry)
XX Ribose-5-Phosphate isomerase cDNA sequence #57.
DE Ribose-5-Phosphate isomerase cDNA sequence #57.
KW Moss; carbohydrate metabolism related protein; GMP; sugar; cofactor;
KW fine chemical production; carbohydrate; polysaccharide; ss.
XX Physcomitrella patens.
OS Physcomitrella patens.
XX WO200144476-A2.
XX
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Query Match 16.3% Score 44.6; DB 21; Length 77536;
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 Matches 95; Conservative 0;

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QY 96 ttcacgcgcacccgagaaagcgcgcacgtgacgcgcgcctcctccacccctccctcc 155
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DB 46291 GCGGAACCTCGCCCACTTCCTACGACTCCGCGCGCGCGCGCGCGCGCGCGCGGAC 46232
QY 216 gagtcgcgcacatgctcctcgcgcctagagcaccgcgcctcaccgcaagatgcgtgcacgcg 274
DB 46231 CACCTCGACGACGAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 46173

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RESULT 9
AAH44089
ID AAH44089 standard; cDNA; 1233 BP.
AC AAH44089;
XX
XX 12-SEP-2001 (first entry)
DE Oryza sativa peroxidase r2329 encoding cDNA SEQ ID NO:37.
XX Oryza sativa; rice; peroxidase; POX; characteristic; gene expression;
KW

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 3, 2002, 07:58:01 ; Search time 796.36 Seconds
(without alignments)
830.042 Million cell updates/sec

Title: US-09-300-482-356
Perfect score: 385
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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23: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	260.2	67.6	477	21	AAC35784 Zea mays DNA fragm
2	170.4	44.3	2629	17	AAT35903 Sequence encoding
3	170.4	44.3	2629	21	AAAT1793 Tobacco transketol
4	162.2	42.1	1681	21	AAC34305 Arabidopsis thalia
5	162.2	42.1	2614	21	AAC36886 Arabidopsis thalia
6	160.6	41.7	700	21	AAC34801 Arabidopsis thalia
7	155	40.3	1839	21	AAC46455 Arabidopsis thalia
8	155	40.3	2226	21	AAC43120 Arabidopsis thalia
9	116.2	30.2	1998	23	AAS54058 Pseudomonas aerugi

10	114.6	29.8	1998	22	AAS00429 Pseudomonas aerugi
11	114.6	29.8	1998	22	AAS00430 Pseudomonas aerugi
12	108.4	28.2	17775	23	AAS59506 Propionibacterium
13	93.8	24.4	2100	22	AAB66705 C. glutamicum codin
14	93.8	24.4	2223	22	AAE71483 Corynebacterium gl
15	93.8	24.4	2350	22	AAS15846 C. glutamicum part
16	93.8	24.4	4108	22	AAE99988 DNA encoding Coryn
17	93.8	24.4	6995	22	AAE25332 Nucleotide sequenc
18	93.8	24.4	6995	22	AAE29332 C. glutamicum Opca
19	93.8	24.4	349980	22	AAH68529 C. glutamicum codin
20	88.6	23.0	2944528	24	ABR03041 Listeria monocytog
21	86.4	22.4	2115	23	AAS56005 Salmonella typhi D
22	82.8	21.5	1992	22	AAH81452 Escherichia coli p
23	82.8	21.5	2143	22	AAD06950 ltkA gene encoding
24	82.8	21.5	6641	22	AAD06957 pME2 comprising ub
25	81.2	21.1	1698	23	AAS94417 DNA encoding novel
26	81.2	21.1	1989	23	AAS44405 staphylococcus aur
27	80.6	20.9	11443	19	AAV52182 Streptococcus pneu
28	80.4	20.9	738	23	AAS89780 DNA encoding novel
29	80.4	20.9	2004	23	AAS52511 E. coli DNA for ce
30	80.4	20.9	2637	23	AAS74812 DNA encoding novel
31	80.4	20.9	2637	23	AAS90091 DNA encoding novel
32	80.4	20.9	3051	23	AAS89789 DNA encoding novel
33	80.4	20.9	4275	23	AAS89787 DNA encoding novel
34	80.0	20.8	1953	18	AAV74685 Staphylococcus aur
35	78.8	20.5	1971	23	AAS1643 Staphylococcus aur
36	78.2	20.3	1968	21	AAC60494 streptococcus pneu
37	78	20.3	1989	21	AAA64393 DNA encoding a Sta
38	76.8	19.9	1998	23	AAS53437 Haemophilus Influe
39	74.4	19.3	48275	21	AAAB1501 N. meningitidis pa
40	74.4	19.3	349980	21	AAE21610 Neisseria meningit
41	74.4	19.3	349980	21	AAE21611 Neisseria meningit
42	74.4	19.3	837096	21	AAAB1489 N. meningitidis pa
43	71	18.4	5348	23	AAS90092 DNA encoding novel
44	67.4	17.5	1996	22	ABA89025 Escherichia coli p
45	67.4	17.5	16066	22	ABA89022 Escherichia coli p

ALIGNMENTS

RESULT 1

AAC35784 ID AAC35784 standard; DNA: 477 BP.

XX AAC35784;

XX 17-OCR-2000 (first entry)

DE Zea mays DNA fragment SEQ ID NO: 11411.

XX Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway; metabolic;

KW pathway; promoter; termination sequence; corn; ss.

OS Zea mays subsp. mays.

XX EP1033405-A2.

PN

XX 06-SEP-2000.

PD

XX 25-FEB-2000; 2000EP-0301439.

PF

XX 25-FEB-1999; 9905-0121825.

PR 05-MAR-1999; 9905-0123180.

PR 09-MAR-1999; 9905-0123548.

PR 23-MAR-1999; 9905-0125788.

PR 25-MAR-1999; 9905-0126264.

PR 29-MAR-1999; 9905-0126785.

PR 01-APR-1999; 9905-0127462.

PR 06-APR-1999; 9905-0128234.

PR 08-APR-1999; 9905-0128714.

PR 16-APR-1999; 9905-0129845.

PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-01300449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
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Matches 268; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 1 caaccgagaccgaagctacatcattggttgaggaccggtccgagctcgagatcgag 60
Db 197 cgaccggaacaagccctgacctcattgagtgaccggtccgagctcgagatcgag 256
OY 61 gcaatgcgagccgagcagctgaggaagagggaggaagcagctccgctcgtctcgtct 120
Db 257 ccaagcgccgagcagcagctgaggaagagggaggaagcagctccgctcgtctcgtct 316
OY 121 cctgggaactctttgtagagcagctcgagatgatacaagagagagcgtccctccgagc 180
Db 317 cctgggaactctttgtagagcagctcgagatgatacaagagagagcgtccctccgagc 376
OY 181 tcacgagcagatcagcagctcagagcgggtccacatcctcgctcgagagatcagcag 240
Db 377 tcacgagcagatcagcagctcagagcgggtccacatcctcgctcgagagatcagcag 436
OY 241 cccaaggaaggaagcattgagcagcagcaagttcgagcagcag 281
Db 437 cccaaggaaggaagcattgagcagcagcaagttcgagcagcag 477

RESULT 2
AA735903
ID AA735903 standard; cDNA; 2629 BP.

AC AA735903;

DT 29-JAN-1997 (first entry)

DE Sequence encoding tobacco transketolase.

KW Transketolase; herbicide; Nicotiana tabacum; identification;
screening; ss.

OS Nicotiana tabacum.

FT Key Location/Qualifiers
CDS 60..2291
/*tag= a

FT /product= Transketolase.

EP723017-A2.

PD 24-JUL-1996.

XX 13-JAN-1996; 96EP-0100458.
XX 23-JAN-1995; 95DE-4001906.
XX (SCHM/) SCHMIDT R.
PA (BADI) BASF AG.
XX Schmidt R, Sonnewald U, Stitt M;
PI WPI: 1996-335478/34.
DR P-PSDB; AAM03319.
PT New transketolase from tobacco and related DNA - useful for
XX screening for inhibitors which are potential herbicides
XX Claim 5; Page 9-12; 26pp; German.
CC The transketolase from tobacco is useful for identifying herbicides
CC for their ability to inhibit the transketolase. The transketolase
CC can be produced in pure form by cloning the gene.
SQ Sequence 2629 BP; 686 A; 595 C; 620 G; 728 T; 0 other;

Query Match 44.3%; Score 170.4; DB 17; Length 2629;
Best Local Similarity 67.4%; Pred. No. 1.8e-33;
Matches 240; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

OY 4 ccggaccacgaagctacatcattggttgaggaccggtccgagctcgagatcgagcagga 63
Db 1936 ctgggaacaacaacctgattgattgattgattgattgattgattgattgattgattgatt 1995
OY 64 atcgagccgagcagctgaggaagagggaggaagcagctccgctcgtctcgtctcct 123
Db 1996 aggcgctgattgattgattgattgattgattgattgattgattgattgattgattgatt 2055
OY 124 ggggaactctttgtagagcagctcgagatgatacaagagagagcgtccctccgagcgtta 183
Db 2056 ggggaactctttgtagagcagctcgagatgatacaagagagagcgtccctccgagcgtta 2115
OY 184 cagcagagcagcagctcagagcgggtccacatcctcgctcgagagagcagcagcagcc 243
Db 2116 cagcagagcagcagctcagagcgggtccacatcctcgctcgagagagcagcagcagcc 2175
OY 244 aaggaaggaagcattgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 303
Db 2176 aaggaaggaagcattgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2235
OY 304 aggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 359
Db 2236 aggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2291

RESULT 3
AAA71793
ID AAA71793 standard; cDNA; 2629 BP.

AC AAA71793;

DT 08-JAN-2001 (first entry)

DE Tobacco transketolase cDNA.

KW Transketolase; tobacco; transgenic plant; tocopherol; Vitamin K; lignin;
chlorophyll; lignin; aromatic amino acid; soya; canola; barley; oat;

KW wheat; rape; maize; sunflower; ss.

OS Nicotiana tabacum.

FT Key Location/Qualifiers
CDS 60..2291
/*tag= a

FT XX /product= "transketolase"
PN XX DE19003493-A1.
PD XX 03-AUG-2000.
XX XX
PF 29-JAN-1999; 99DE-1003493.
XX XX
PR 29-JAN-1999; 99DE-1003493.
XX XX
PA (BADI) BASF AG.
XX XX
PI Henkes S, Badur R, Nigel MS, Schmidt R, Reindl A, Zrenner R;
XX XX WPI: 2000-533873/49.
DR P-PSDB: AAB10624.
XX XX
PT Novel transgenic plant containing gene for transketolase, with
PT increased content of e.g. tocopherol, chlorophyll or aromatic amino
PT acids
XX XX
PS Example 1: Page 19-23; 36pp; German.
XX XX
CC This invention describes the novel use of DNA (1) encoding a
CC transketolase (II) to prepare plants (A) with increased content of
CC tocopherols, vitamin K, chlorophyll, lignin and/or aromatic amino acids.
CC The method is used to produce transgenic soya, canola, barley, oats,
CC wheat, rape, maize or sunflower with increased contents of tocopherols,
CC vitamin K, chlorophyll, lignin and/or aromatic amino acids. The plants
CC also have increased resistance to transketolase inhibitors. This sequence
CC encodes the Nicotiana tabacum (tobacco) transketolase protein which is
CC used in the method of the invention.
XX XX
SQ Sequence 2629 BP; 686 A; 595 C; 620 G; 728 T; 0 other;

Query Match 44.3%; Score 170.4; DB 21; Length 2629;
Best Local Similarity 67.4%; Pred. No. 1.8e-33;
Matches 240; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 4 ccggacacaaagcctgacatcatctgggttggcgccgctccgagctggaatcggggca 63
DB 1936 cgggacaacaacctgacatcttgcattgtctgactgctcagatgtagaattgctgtca 1995
QY 64 atgcgacgcagcagctggaaggaagggaagcgttcgcgctgctcgttcgtcgtcctc 123
DB 1996 aggcctcgtgatgaactcaggaagaaggaagcgtgagatgttctccttctgtc 2055
QY 124 ggggaactcttgatgagcagctcgatgagttacaagagagcgttcctcctcgcgacgtca 183
DB 2056 gggagctcttctgaaagacaatcagccgactacaagaaagtctcctcatcatctgtta 2115
QY 184 cagcgaggaatcagcagctcgagcggctgcacttcggctggcgagaaagatcggaagccc 243
DB 2116 cagctagagtttagcatttgaggcgccgacatccacttgggtgggaaataatctcgataaa 2175
QY 244 aaggcaaggccatttgcgacgaagtcgcggcgagatgcttcctgcggagcgaatcaca 303
DB 2176 aggggaagagccatcggaattgcacagatgggtgtgccagtgccctcctgtaaaatatataca 2255
QY 304 aggaatcagcagcagctgagagacatcatctgcaactgccaagaagcctttaagag 359
DB 2236 aggaatcaggaattaccagcagaagcgtgtgtgtagctgcagccaacaagaattcttaag 2291

RESULT 4
ID AAC34305 standard; DNA; 1681 BP.
XX AAC34305;
AC AAC34305;
XX
DT 17-OCT-2000 (first entry)
XX

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 6175.
XX XX Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX XX
OS Arabidopsis thaliana.
XX XX
PN EP1033405-A2.
XX XX
PD 06-SEP-2000.
XX XX
PF 25-FEB-2000; 2000EP-0301439.
XX XX
PR 25-FEB-1999; 99US-0121825.
XX XX 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
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PR 11-MAY-1999; 99US-0134256.
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QY 184 cagcgagatcacgatacgagcggtgtccactctcgtgtcgagagaagatcgagagccc 243
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QY 244 aagcgaagcgcatcgacatcgacaaagttcggcgagagtcctcccgagacatctaca 303
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RESULT 5
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XX 17-OCT-2000 (first entry)
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XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
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RESULT 6
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DT 17-OCT-2000 (first entry)
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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147302.
PR 06-AUG-1999; 99US-0147302.
PR 09-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 10-AUG-1999; 99US-0147935.
PR 11-AUG-1999; 99US-0148171.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148565.
PR 16-AUG-1999; 99US-0148684.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151458.
PR 01-SEP-1999; 99US-0151950.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155139.
PR 24-SEP-1999; 99US-0155486.
PR 28-SEP-1999; 99US-0155659.
PR 29-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 08-OCT-1999; 99US-0158369.
PR 12-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
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PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
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PR 21-OCT-1999; 99US-0160741.
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PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
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PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 23-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.

PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.
PR 29-OCT-1999; 99US-0162143.

Query Match	40.3%	Score 155;	DB 21;	Length 1839;
Best Local Similarity	65.4%;	Pred. No. 1.2e-29;		
Matches 227; Conservative	0;	Mismatches 120;	Indels 0;	Circ 0

QY 1 caaccgycaccaagcctacatcatgttggtggcacccgcctcgagctggagatcgcg 60
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QY 61 gcaatgcgcccgaagctgtgaaggaggagaacggtccgctcgttcgtrt 120
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Db 1541 ctcaagctgcagaaagttaacgacaacagggcaaatrtnaaat+++++ttttttt 1500

Oy 121 ccctgggaactccttgcagacgagtcggaatgatacaaggagagcgctccctccgcgcgacg 180
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Db 1601 gttggagaaccttctgcacacgacatcacatatcacaanaaaaaattatcttccccctctctcta 1660

Dy 181 tcacagcgaagtatcagcatcgagccgggtcccactcttcgcttgcagaagtactgcgag 240
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Db 1661 taccagctaagattaatctcgaagctccaacctttttagatgaaataaatttatctaaa 1720

DY 241 cccaagcgaagccatgcatcgacaagtctgcgcgagtcctctccggaacgatct 300
||||| | | ||||| | | | | | | | | | | | |
Db 1721 gaaaagggaattcgaattgaatacgtttggaaacaaotrcacacgacgaaaacct++ 1760

OY 301 acaaagagatcagcatccacgctggagaagcatcattgcactccaag 347
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Db 1781 ataaagagtcttgatatcaccaattgaagctatgaattaaaccaccaa 1827

RESULT 8
AAC43120

XX	
AC	AAC43120;
XX	

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 38100.

protein identification; signal transduction pathway;
metabolic pathway; promoter; termination sequence; ss.

XX
PN
XX
EP1033405-A2.

XX
PF 25-FEB-2000; 2000EP-0301439.
XX

PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.

PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
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PR 21-APR-1999; 99US-0130449.
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PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
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PR 01-JUN-1999; 99US-0137222.
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PR 16-JUN-1999; 99US-0139452.
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PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
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PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141847.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
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PR 06-AUG-1999; 99US-0147303.
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PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
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PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
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PR 27-AUG-1999; 99US-0151080.
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PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
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PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158366.
PR 13-OCT-1999; 99US-0159293.

QY 311 cggcatcacgctggagagcatcattgcacatgcacgaag 347
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Db 1944 cggcttcacctgtgacaacgctcctgcyggtgcccgaag 1980

RESULT 10
AAS00429
ID AAS00429 standard; DNA; 1998 BP.

AC AAS00429;

DT 11-MAY-2001 (first entry)

DE Pseudomonas aeruginosa transketolase tkta gene.

KW Transketolase; tkta; microbial growth; antimicrobial; antibacterial;
bacterial infection; gastric ulcer; chronic lung infection; gastritis;
cystic fibrosis; microbial disease; Helicobacter pylori infection;
KW gastrointestinal carcinoma; endocarditis; bacteraemia; pneumonia;
osteomyelitis; otitis media; urinary tract infection; folliculitis; ds.

OS Pseudomonas aeruginosa.

FH Key Location/Qualifiers

FT CDS

1..1998

FT /*tag= a

/product= "tkta protein"

PN W0200114523-A1.

PD 01-MAR-2001.

PE 16-AUG-2000; 2000WO-US22324.

PR 24-AUG-1999; 99US-0382106.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Huang J, Jiang X, McDevitt D, Van Horn S;

DR WPI: 2001-218437/22.

DR P-PSDB; AAU00425.

PT New Pseudomonas aeruginosa tkta polypeptide and polynucleotide, useful
for screening antibacterial compounds for treating microbial diseases,
PT and as diagnostic reagents for diagnosing or prognosing bacterial
infection -

PS Claim 2; Page 3; 40pp; English.

CC The present sequence encodes for a novel Pseudomonas aeruginosa
transketolase tkta protein which is related to other proteins of the
transketolase family. The tkta protein is essential for the growth
and/or survival of P. aeruginosa or any organism that may possess it.
CC This is shown in particular by a temperature sensitive (ts) mutant
ts-92 (AAU00426) which has an amino acid substitution of Arg to His at
residue 204. The tkta polypeptides are useful as antimicrobial
CC particularly antibacterial compounds and identifying membrane bound or
soluble receptors. The tkta polynucleotides can be used as diagnostic
reagents. Both the tkta polypeptides and polynucleotides are useful for
diagnosing or prognosing a disease or susceptibility to a disease in a
human (e.g. bacterial infection) and for assessing the binding of small
CC molecule substrates and ligands in cells and chemical libraries. Diseases
caused by P. aeruginosa are difficult to treat because of antibiotic
resistance and untreatable strains often found in patients with chronic
lung infections e.g. cystic fibrosis. The agonists and antagonists to
CC the tkta polypeptides and polynucleotides are useful for treating
microbial diseases such as endocarditis, bacteraemia, pneumonia, otitis,
CC osteomyelitis, folliculitis and urinary tract and wound infections.
CC Helicobacter pylori infections, reducing the risk of H. pylori-induced
cancers such as gastrointestinal carcinoma and also preventing/treating
gastric ulcers and gastritis.

XX SQ Sequence 1998 BP; 365 A; 710 C; 636 G; 287 T; 0 other:

Query Match 29.8%; Score 114.6; DB 22; Length 1998;
Best Local Similarity 58.8%; Pred. No. 1,8e-19;
Matches 198; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

QY 11 caagctgacacatcttggttgcgaccggtccgagctggagatcgcggacaatgcggc 70
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Db 1644 cgagccggaactgattcctcgtacgcacccggttcggaagtcggctgcgcgcgccta 1703
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QY 71 cgaagcgtgaggaagagggggaagacggtccggtcgtctcgtctcctccttggaaact 130
|||||

Db 1704 cgaagagctcagcgagccagcgccgaaggtccggtgtgctatgcatagcaccagcgt 1763
|||||

QY 131 cttagatgagcagtcgagtgatcaagaagagcgctccctccctccgacgctcaagcgag 190
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Db 1764 ctacgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1823
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QY 191 gatacagcatcgagcgccgggtccactctcgtctggcagaagtcagtcggagcccaagcga 250
|||||

Db 1824 catcgccatcgagcgccgcccatcgccgactactgttacaagtcagtcggtctcgacggcg 1883
|||||

QY 251 ggcattgagcatcgacaagtcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 310
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Db 1884 catcatcgcatgacacagcttcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcact 1943
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QY 311 cggcatcacgctggagagcatcattgcacatgcacgaag 347
|||||

Db 1944 cggcttcacctgtgacaacgctcctgcyggtgcccgaag 1980

RESULT 11

AAS00430
ID AAS00430 standard; DNA; 1998 BP.

AC AAS00430;

DT 11-MAY-2001 (first entry)

DE Pseudomonas aeruginosa transketolase tkta mutant ts-92 DNA.

KW Transketolase; tkta; microbial growth; antimicrobial; antibacterial;
bacterial infection; gastric ulcer; chronic lung infection; gastritis;
KW cystic fibrosis; microbial disease; Helicobacter pylori infection;
KW gastrointestinal carcinoma; mutant; mutuin; endocarditis; bacteraemia;
KW pneumonia; osteomyelitis; otitis media; urinary tract infection;
folliculitis; ds.

OS Pseudomonas aeruginosa.

OS Synthetic.

FH Key Location/Qualifiers

FT CDS

1..1998

FT /*tag= a

/product= "tkta mutant ts-92"

FT mutation

replace (611,6)

FT W0200114523-A1.

PD 01-MAR-2001.

PE 16-AUG-2000; 2000WO-US22324.

PR 24-AUG-1999; 99US-0382106.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PI Huang J, Jiang X, McDevitt D, Van Horn S;

DR WPI: 2001-218437/22.
P-PSDB: AAU00426.

PT New Pseudomonas aeruginosa tkta polypeptide and polynucleotide, useful
PT for screening antibacterial compounds for treating microbial diseases,
PT and as diagnostic reagents for diagnosing or prognosing bacterial
PT infection

PS Example 2: Page -: 40pp: English.

CC The present sequence encodes for Pseudomonas aeruginosa transketolase
CC tkta mutant ts-92 protein. A novel P. aeruginosa tkta protein which is
CC related to other proteins of the transketolase family is essential for
CC the growth and/or survival of P. aeruginosa or any organism that may
CC possess it. This is shown in particular by the temperature sensitive
CC (ts) mutant ts-92 (AAU00426) which has an amino acid substitution of Arg
CC to His at residue 204. The tkta polypeptides are useful as antimicrobial
CC particularly antibacterial compounds and identifying membrane bound or
CC soluble receptors. The tkta polynucleotides can be used as diagnostic
CC reagents. Both the tkta polynucleotides and polynucleotides are useful for
CC diagnosing or prognosing a disease or susceptibility to a disease in a
CC human (e.g. bacterial infection) and for assessing the binding of small
CC molecule substrates and ligands in cells and chemical libraries. Diseases
CC caused by P. aeruginosa are difficult to treat because of antibiotic
CC resistance and untreatable strains often found in patients with chronic
CC lung infections e.g. cystic fibrosis. The agonists and antagonists to
CC the tkta polypeptides and/or polynucleotides are useful for treating
CC microbial diseases such as endocarditis, bacteraemia, pneumonia, otitis,
CC osteomyelitis, folliculitis and urinary tract and wound infections.
CC Helicobacter pylori infections, reducing the risk of H. pylori-induced
CC cancers such as gastrointestinal carcinoma and also preventing/treating
CC gastric ulcers and gastritis.
CC Note: The present sequence is not given in the patent but is indexed from
CC the wild type sequence.

SQ Sequence 1998 BP; 366 A; 710 C; 635 G; 287 T; 0 other;

Query Match 29.8%; Score 114.6; DB 22; Length 1998;
Best Local Similarity 58.8%; Pred. No. 1.8e-19;

Matches 198; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

QY 11 caagctgcatcatgtggttgggacgcgctcgcagctgagatcgcggacatgcggc 70
DB 1644 cgaagccggaactgctctatcgcgcacgcgttcggaagtcggcctggcgtgacgcta 1703
QY 71 cgaagctgaggaagaggaagagacggctcgcgtctgctcgtctcctctgggaact 130
DB 1704 cgaagctcagcagcagcggcgcaaggtccgcgtggtatcgatgcattgcaccagcgt 1763
QY 131 cttgatgacgactcgatgagtaacaaagagagctcctcctgcgcagctcacaagcgag 190
DB 1764 ctacagcagcagcagcagctcctacacagacgtcgtgctgcggtggaagtcggcgcg 1823
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DB 1824 catcgcatcgaagcggcgcccatgcgcgaactactggtacaaagtaagtcgctcgcg 1883
QY 251 ggcacatgcatcgaagaagtcgcgcgagtcctcctcgcggagccgtacaaagagta 310
DB 1884 catcctgcagcatgaccagcttcgcgcgagtcggcgcggcccgccgctgctcgagcact 1943
QY 311 cggcagcagctgagagcattcattgcgaactgcgaag 347
DB 1944 cggctcacctcgacacagctctcgtcggtggcgag 1980

RESULT 12
AAS59506
ID AAS59506 standard; DNA: 17775 BP.
XX
AC AAS59506;
XX

DT 13-FEB-2002 (first entry)

DE Propionibacterium acnes immunogenic protein encoding DNA #1.

KW SAPHO syndrome; synovitis; acne; pustulosis; hyperostosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant; ds.

OS Propionibacterium acnes.

PN WO200181581-A2.

PD 01-NOV-2001.

PF 20-APR-2001; 2001WO-US12865.

PR 21-APR-2000; 2000US-199047P.

PR 02-JUN-2000; 2000US-208841P.

PR 07-JUL-2000; 2000US-216747P.

PA (CORI-) CORIXA CORP.

PI Skeiky YAM, Persing DH, Mitcham JT, Wang SS, Bhatia A;

PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

DR WPI: 2001-616774/71.

PT Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris

PS Claim 1; SEQ ID NO 1; 1069pp: English.

CC Sequences AAS59506-AAS59804 represent DNA molecules encoding
CC Propionibacterium acnes immunogenic polypeptides. The proteins and their
CC associated DNA sequences are used in the treatment, prevention and
CC diagnosis of medical conditions caused by P. acnes. The disorders include
CC SAPHO syndrome (synovitis, acne, pustulosis, hyperostosis and
CC osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved
CC in infections of bone, joints and the central nervous system, however it
CC is particularly involved in the inflammatory lesions associated with acne
CC vulgaris. A method for detecting the presence or absence of P. acnes in a
CC patient comprises contacting a sample with a binding agent that binds to
CC the proteins of the invention and determining the amount of bound protein
CC in the sample. The polypeptides may be used as antigens in the production
CC of antibodies specific for P. acnes proteins. These antibodies can be
CC used to downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA). This sequence encodes the
CC polypeptides shown in AAU39105-AAU39296, AAU67455 and AAU67456.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 17775 BP; 3406 A; 5404 C; 5475 G; 3487 T; 3 other;

Query Match 28.2%; Score 108.4; DB 23; Length 17775;
Best Local Similarity 58.3%; Pred. No. 9.9e-18;
Matches 190; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

QY 7 gaccaaagcctgacatcatcgtgttggaacgcgctcgcagctggaatcgcggaatg 66
DB 11159 ggcgcgagcccaagaatcatcctcctcgtactggttcgcgcgctgctgcgaag 11218
QY 67 cggcgcagcagctgaggaaggaaggaagcgtccgcgtcgtcgtcgtcgtcgtcgtg 126
DB 11219 cagcgaggaagcttgagcgcgaggaatcgacccgcgtcgtcgtgagtcgtgcgaag 11278
QY 127 aactcttgatgacagctcgatgatacaaggaagcgtccctcctgcgcagctacag 186

Query Match

Db 11279 agtggttcagacgaggcaagcgagtaglaccgcgaatcgttgtacctaccacgatctagtacty 11338
OY 187 cgaagcatcacataccgagccgggttcactctcggcttgvcagaagtacgtcggaaaccaag 246
DB 11339 ccgcagattgagcgctcgagggcccgcgcacatgcccalgtgcggacaagtaigtctgcgcgaag 11398
OY 247 gcaaagccaattggcatalcgcgaaatgcgcgcgaagtctctctccggagcatctacaag 306
DB 11399 gcgcctcgtgtccccctcgcgcgaacttcgcgcgcctccgcctcttgsggcgctgtctgcaga 11458
OY 307 agtacgcataccctgtgagagatc 332
DB 11459 agtccgattcacccgtgaccacgctc 11484

RESULT_13

AHH6705
ID AHH6705 standard; DNA; 2100 BP.
XX
AC AAH6705;
XX
DT 26-SEP-2001 (first entry)
DE C glutamicum coding sequence fragment SEQ ID NO: 1740.
XX
KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
organic acid synthesis; ds.
XX
OS Corynebacterium glutamicum.
PN EP1108790-A2.
PD 20-JUN-2001.
PE 18-DEC-2000; 2000EP-0127688.
PR 16-DEC-1999; 99JP-0377484.
PR 07-APR-2000; 2000JP-0159162.
PR 03-AUG-2000; 2000JP-0280988.
XX
PA (KIOWA) KIOWA HAKKO KOGYO KK.

P1 Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda W, Ozaki A;
DR WPT: 2001-376931/40.
DK P-PADB; AAG91486.

PP Novel polynucleotides derived from Coryneform bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analysing
PI expression profile or pattern of a gene and identifying homologous gene
PX -
PS Claim 8; SEQ ID NO: 1740; 246pp + Sequence Listing; English.
XX
CC The present invention provides a number of nucleotide and protein
sequences from the Coryneform bacterium Corynebacterium glutamicum. These
are useful for identifying the mutation point of a gene derived from a
mutant of Coryneform bacterium, measuring expression amount and
analysing the expression profile or expression pattern of a gene derived
from Coryneform bacterium, and identifying a homologue of a gene derived
from Coryneform bacterium. Coryneform bacteria are useful for producing
amino acids, nucleic acids, vitamins, saccharides and organic acids,
particularly L-Lysine. The present sequence is a nucleic acid described
in the exemplification of the invention.
CC Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from the
European Patent Office.
CX
SO Sequence 2100 BP; 407 A; 650 C; 580 G; 463 T; 0 other;

	Best Local Similarity	54.9%;	Pred. NO. 3e-14;	
	Matches 185;	Conservative	0;	Mismatches 152; Indels 0; Gaps 0;
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Dd	1753	ccagaatgatcccatcgaatggctccggctccgaagtccaacttgcagtaaccgtgcgaag	1812	
QY	75	gaagctagaagaagaggagaaagacggtccgcgtctgtctgtctcgttcctctggaactcttt	134	
Dd	1813	gctcttgtgaagcctcgaggcgcttgcagctcgtctgtttccgttcctctgcatgtattgttc	1872	
QY	135	gatygacagctcgatgatgataacaagagagcgtccctccctccgacgcaacagcgaagtc	194	
Dd	1873	csagagcagacgacgaagagatacatcgatcgtcttcgtccgtcacgctgtgacctcgttg	1932	
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QY	255	attggatcgacaagttgcgcgagtgctcctccgagacatcataaagagtagcgc	314	
Dd	1993	gtctcccttgacactcgtcggtctcttcgcgattaccaaacctgttgagaagltcgac	2052	
QY	315	atcacccgtgagaagacatcatctgcaactgcgaagaagct	351	
Dd	2053	atcacaccgatcgactcgttgccagcgccgaaggaact	2089	
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ID	AAF71483	standard; DNA; 2223 BP.		
XX	AC	AAE71483;		
XX	DT			
XX	30-APR-2001	(first entry)		
Corynebacterium glutamicum SMP protein nucleotide sequence SEQ ID NO:247.				
XX				
KW	Corynebacterium glutamicum; carbon metabolism and energy production;			
KW	SMP protein; sugar metabolism and oxidative phosphorylation protein;			
KW	non-chemical production; organic acid; proteinogenic amino acid;			
KW	famine biochemical product; purine base; pyrimidine base; nucleoside;			
KW	nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;			
KW	carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;			
KW	diagnosis; Corynebacterium diptheriae; evolutionary study; ds.			
OS	Corynebacterium glutamicum.			
PN	WO200100844-A2.			
PD	04-JAN-2001.			
PF	23-JUN-2000; 2000WO-TB00943.			
XX				
XX	25-JUN-1999; 99DS-0141031.			
PR	08-JUL-1999; 99DE-1031412.			
PR	08-JUL-1999; 99DE-1031413.			
PR	08-JUL-1999; 99DE-1031419.			
PR	08-JUL-1999; 99DE-1031420.			
PR	08-JUL-1999; 99DE-1031424.			
PR	08-JUL-1999; 99DE-1031426.			
PR	08-JUL-1999; 99DE-1031431.			
PR	08-JUL-1999; 99DE-1031433.			
PR	08-JUL-1999; 99DE-1031434.			
PR	08-JUL-1999; 99DE-1031510.			
PR	08-JUL-1999; 99DE-1031562.			
PR	08-JUL-1999; 99DE-1031634.			
PR	08-JUL-1999; 99DE-1032180.			
PR	08-JUL-1999; 99DE-1032227.			
PR	08-JUL-1999; 99DE-1032230.			
PR	09-JUL-1999; 99US-0143208.			
PR	14-JUL-1999; 99DE-1032924.			
PR	14-JUL-1999; 99DE-1032973.			

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 3, 2002, 08:11:28 ; Search time 185.98 Seconds
(without alignments)
508.490 Million cell updates/sec

Title: US-09-300-482-356

Perfect score: 385
Sequence: 1 caaccgcacccaagcctgac.....acggtctggaggtttttt 385

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/PCITUS.COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	170.4	44.3	2629	2 US-09-012-030-1	Sequence 1, Appli
2	170.4	44.3	2629	2 US-08-590-454-1	Sequence 1, Appli
3	114.6	29.8	1998	4 US-09-382-106-1	Sequence 1, Appli
4	82.8	21.5	2143	4 US-09-064-693A-18	Sequence 18, Appli
5	82.8	21.5	6641	4 US-09-064-693A-25	Sequence 25, Appli
6	78.2	20.3	1968	4 US-09-298-724-1	Sequence 1, Appli
7	76.8	19.9	1995	5 PCT-US96-05320A-1025	Sequence 1025, Ap
8	63	16.4	1738	4 US-08-858-207A-35	Sequence 35, Appli
9	51.6	13.4	1872	2 US-08-743-637B-17	Sequence 17, Appli
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11	44	11.4	1284	4 US-09-327-487A-4	Sequence 4, Appli
12	43	11.2	1281	4 US-09-327-487A-3	Sequence 3, Appli
13	43	11.2	2872	4 US-09-327-487A-2	Sequence 2, Appli
14	41.2	10.7	4195	1 US-08-360-011-1	Sequence 1, Appli
15	41.2	10.7	4195	3 US-08-901-710-1	Sequence 1, Appli
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17	41.2	10.7	4425	1 US-08-222-616-31	Sequence 31, Appli
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21	41.2	10.7	9108	5 PCT-US95-04228-45	Sequence 45, Appli
22	41	10.6	1693	3 US-09-320-878-23	Sequence 23, Appli
23	37	9.6	71989	4 US-09-443-501A-2	Sequence 2, Appli
24	36.6	9.5	4403765	4 US-09-103-840A-2	Sequence 1, Appli
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26	36.2	9.4	1931	2 US-09-130-114-2	Sequence 2, Appli
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30	35.6	9.2	1632	1 US-08-259-924-1	Sequence 1, Appli
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33	35.4	9.2	68750	3 US-09-335-409-1	Sequence 1, Appli
34	35.4	9.2	68750	4 US-08-568-102-1	Sequence 1, Appli
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37	35.4	9.2	68750	4 US-09-568-486-1	Sequence 1, Appli
38	35.4	9.2	68750	4 US-09-568-472-1	Sequence 1, Appli
39	35.2	9.1	711	4 US-09-651-941-22	Sequence 18, Appli
40	35.2	9.1	711	4 US-09-651-941-22	Sequence 22, Appli
41	35.2	9.1	12508	4 US-09-651-941-1	Sequence 1, Appli
42	35.2	9.1	12523	4 US-09-651-941-1	Sequence 1, Appli
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44	34.8	9.0	1029	4 US-09-449-437A-1	Sequence 1, Appli
45	34.8	9.0	2238	1 US-08-742-011-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-012-030-1
Sequence 1, Application US/09012030
Patent No. 5912169
GENERAL INFORMATION:
APPLICANT: SCHMIDT, Ralf-Michael, STITT, Marc, SONNEWALD,
APPLICANT: Uwe
TITLE OF INVENTION: Transketolase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Keil & Weinlauf
STREET: 1101 Connecticut Avenue
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM AT-compatible, 80486 processor
OPERATING SYSTEM: MS-DOS version 6.0
SOFTWARE: Wordperfect version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012.030
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,454
FILING DATE: 22-JAN-1996
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2629 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE: Nicotiana
ORGANISM: Nicotiana
FEATURE:
NAME/KEY: CDA
LOCATION: 60..2289
US-09-012-030-1

Query Match 44.3%; Score 170.4; DB 2; Length 2629;
Best Local Similarity 67.4%; Pred. No. 6.8e-37;
Matches 240; Conservative 0; Mismatches 116; Indels 0; Gaps 0;
OY 4 ccgcgcacccaagcctgacatctgtgtggcaccgctccgcgcgtgagatccgggca 63
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Db	1936	CTGGCAACAAACGATGTCATATTTTGATTGGTACGTGGCTACAGATTGAAATTTGCTGTCA	1935
OY	64	atgagcgccgaagagctctgaagaagagaggagaacggtccgcgcgtcgcattcgcctcc	123
Db	1996	AGCGCTCGATGAACTCTCAGGAAAAGAGAAAGACATGTGAGATGTTCTCTTGTGTGT	2055
OY	124	gggaacctcttgatgagcaatcgcatgtagtacaagaagagagctctccctgcgaagca	183
Db	2056	GGGAGCTTTTGGAAAGAACATCAGCGACCTACAGAGAAAGTCTCTTCATCATCTGTTA	2115
OY	184	cagagagagatcacacatcggagggccgggtccactctcggtctgcagaagaatcgcgaagcc	243
Db	2116	CAGCTAAGTTAGTATGAAAGCCGGATCCACATTTGGGTGGAGAAATATCTCGATCAA	2175
OY	244	aagggcaagccatttgcattgcatacgaacaaattcgggcgagttctcctccggagcgatcaca	303
Db	2176	AGGGGAAAGCCCATCGGAATTTGACAGATGGGGTGGCCAGTGCCCTCTGGAATAATATACA	2235
OY	304	aggaagtcaggcatcacccggaggagagatcatctgcaactgcgcaagaagctttaagag	359
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RESULT      2
US-08-590-454-1
: Sequence 1, Application US/08590454
: Patent No. 592535
:
GENERAL INFORMATION:
: APPLICANT: SCHMIDT, Ralf-Michael, STITT, Marc, SONNENWALD,
: APPLICANT: Uwe
: TITLE OF INVENTION: Transketolase
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Kell & Weinlauf
: STREET: 1101 Connecticut Avenue
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20036
:
COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
: COMPUTER: IBM AT-compatible, 80486 processor
: OPERATING SYSTEM: MS-DOS version 6.0
: SOFTWARE: Wordperfect version 5.1
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CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/590,454
: FILING DATE: 22-JAN-1996
: CLASSIFICATION: 435
: INFORMATION FOR SEQ. ID NO. 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2629 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHETICAL: NO
: ORIGINAL SOURCE:
: ORGANISM: Nicotiana
:
FEATURE:
: NAME/KEY: CDA
: LOCATION: 60..2289
:
US-08-590-454-1

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Query Match	44.3%	Score 170.4;	DB 2;	Length 2629;
Best Local Similarity	67.4%;	Pred. No. 6.8e-37;		
Matches 240; Conservative	0;	Mismatches 116;	Totals 0;	Coverage 0

[illegible]

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D8	GGGACCTTTTGAAGAAACATACGCCGACATCAAGGAAAAGTCCCTTCATCATCTGTTA	2115
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QY	AAGGCAAGCCATCGATCGACAAGTCTCGCGCGAGTCTCTCTCGGAGCGCTACAA	303
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QY	AGGAGTACGATCAACGTTGAGAGATCATATCGAACGTCGCAAGAGCTTTAAGAG	359
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RESULT      3
US-09-382-106-1
: Sequence 1, Application US/09382106
: Patent No. 6221531
: GENERAL INFORMATION:
: APPLICANT: Huang, Jiansheng
: APPLICANT: Jiang, Xinhua
: APPLICANT: McDevitt, Damien
: APPLICANT: Van Horn, Stephanie
: TITLE OF INVENTION: TKTA
: FILE REFERENCE: GM10236
: CURRENT APPLICATION NUMBER: US/09/382,106
: CURRENT FILING DATE: 1999-08-24
: NUMBER OF SEQ. ID NOS.: 2
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ. ID NO. 1
: LENGTH: 1998
: TYPE: DNA
: ORGANISM: Pseudomonas aeruginosa
US-09-382-106-1

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Query Match	29.8%	Score 114.6	DB 4	Length 1996
Best Local Similarity	58.8%	Pred. No. 66-22		
Matches 198	Conservative	0	Mismatches 139	Indels 0
			Gaps	0
QY 11	caagcctgaacatcatgtgggtctgggacacgcgcgtctccgcgcgtcgagagatccgagcaatgcgcgc	70		
Db 1644	cgcgcgcgggaactcgtatccctatccgcacgcgcgtctcggaagctcgcgcgtcgcgttcgaagcctcta	1703		
QY 71	cgaacgaactgaagaaagagagaggaagacgcgtctccgcgcgtcgtctcgtctcgtctcgtcggaaact	130		
Db 1704	cgcacaagctcgaagacagcagcgcgcgaagctccgcgcgtgtagatcgaatgacatgacacgaacgcgt	1763		
QY 131	ctcttgtagcgctcgtgtagatgacagaagaaagcgtctccctccctgcacgaactacacgcgag	190		
Db 1764	ctacagcgcagcagcagcagcagatctcctaagaagacgcgtctgctgcgcgtctggaagtctgcgcgcg	1823		
QY 191	gattcaacatcagaagccgcggtctccactctcgtcgtcgagaaagtagtcgtccggagccccaaagcga	250		
Db 1824	catcgccatcgcgagccgcgccacatgcgcgcgtactacgtgtacaagaatcgcgtctctcgaagggcgc	1883		
QY 251	ggcccaattgcatcgaacaaagtctcgccgcgcgaatgctctcctcgcggaagatctcaagaagtagta	310		
Db 1884	catctatcgcgcatagaacacagctctcgcgcgaatctgcgcgcgcgcgcgcgcgcgcgcgtctcgcgacatt	1943		
QY 311	cggatccaccgtgtgagagacatcatctgcaacatgcgaag	347		
Db 1944	cggcttcaaccctgcgaacacgtctcgtcgcgtgagcgcgag	1980		

RESULT 4
US-09-064-693A-18

Sequence 18, Application US/09064693A
Patent No. 6210937
GENERAL INFORMATION:
APPLICANT: Ward, Thomas E.
TITLE OF INVENTION: DEVELOPMENT OF GENETICALLY
ENGINEERED BACTERIA FOR PRODUCTION
OF A SPECIFIC PLASTICS PRECURSOR
TITLE OF INVENTION: OF A SPECIFIC PLASTICS PRECURSOR
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: W. Gary Goodson
ADDRESS: INBEL--Lockheed Martin Idaho
ADDRESSEE: Technologies Co.
STREET: P.O. Box 1625
CITY: Idaho Falls
STATE: Idaho
COUNTRY: USA
ZIP: 83415-3810
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
COMPUTER: Toshiba Satellite Pro T2150CDS
OPERATING SYSTEM: Windows95
SOFTWARE: Word Perfect 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,693A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: W. Gary Goodson
REGISTRATION NUMBER: 22,387
REFERENCE/DOCKET NUMBER: LIT-PI-296
TELECOMMUNICATION INFORMATION:
TELEPHONE: (208)526-9469
TELEFAX: (208)526-8339
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2143 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-064-693A-18

	Query Match	21.5%	Score 82.8	DB 4	Length 2143
	Best Local Similarity	53.0%	Pred. No.2,1e-13		
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QY	253	ccattgcatctgcacaagtctcggtcgagtgctctctcgtccgggaacgaatctacaagaagtacg	312		
Db	1866	TCTGTGGTATGACACACTTTCGGTGAATCTGCTCCGGCAGAGCTGCTGTTGAAGAGTTGG	2025		
QY	313	gcataccgctgagagatcatcattgcaactgcgca	346		
Db	2026	GCTTCATGTTGATTAACGTTGTGGGAAGCAAA	2059		

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1      RESULT      5
2      US-09-064-693A-25
3      ; Sequence 25, Application US/09064693A
4      ; Patent No. 6210937
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Ward, Thomas E.
7      ; TITLE OF INVENTION: DEVELOPMENT OF GENETICALLY
8      ; TITLE OF INVENTION: ENGINEERED BACTERIA FOR PRODUCTION
9      ; TITLE OF INVENTION: OF A SPECIFIC PLASTICS PRECURSOR
10     NUMBER OF SEQUENCES: 26
11
12     CORRESPONDENCE ADDRESS:
13     ADDRESSEE: W. Gary Goodson
14     ADDRESSEE: INBEL--Lockheed Martin Idaho
15     ADDRESSEE: Technologies Co.
16     STREET: P.O. Box 1625
17     CITY: Idaho Falls
18
19     STATE: Idaho
20
21     COUNTRY: USA
22     ZIP: 83415-3810
23
24     COMPUTER READABLE FORM:
25     MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
26     COMPUTER: Toshiba Satellite Pro T2150CDS
27     OPERATING SYSTEM: Windows95
28     SOFTWARE: Word Perfect 7.0
29
30     CURRENT APPLICATION DATA:
31     APPLICATION NUMBER: US/09/064,693A
32
33     FILING DATE:
34     CLASSIFICATION: 435
35     PRIOR APPLICATION DATA:
36     APPLICATION NUMBER:
37
38     FILING DATE:
39
40     ATTORNEY/AGENT INFORMATION:
41     NAME: W. Gary Goodson
42     REGISTRATION NUMBER: 22,387
43     REFERENCE/DOCKET NUMBER: LIT-PI-296
44     TELECOMMUNICATION INFORMATION:
45     TELEPHONE: (208)526-9469
46     TELEFAX: (208)526-8339
47
48     INFORMATION FOR SEQ ID NO: 25:
49     SEQUENCE CHARACTERISTICS:
50     LENGTH: 6641 base pairs
51     TYPE: nucleic acid
52     STRANDEDNESS: double
53     TOPOLOGY: linear
54
55     US-09-064-693A-25

```

Query Match	21.5%;	Score 82.8;	DB 4;	Length 6641;
Best Local Similarity	53.0%;	Pred. No. 3e-13;		
Matches 177;	Conservative 0;	Mismatches 157;	Indels 0;	Gaps 0;
QY 13	agccctgacatcalttggtcttggtgacacgcgcgtccgcagctggaatcgcgggcaatgcgcgcg	72		
Db 3768	AGCGGAACTGATTTTTCATCGCTACCGGTTTGAAGTTGAACCTGGCTTCTGCTCAAGC	3827		
QY 73	acgagctgaagaaaggaaggaagaacgcgtccgcgttcgtctcgtctccttggaaactct	132		
Db 3828	AAAACTGACTGCGCGAAGCGCTGAAGCGCGCGTGTGTCATGTCGTCACGACGCAT	3887		
QY 133	ttgatgagcaatcgtgtagtagtacaagagagagcgtctccctcgcgcgaagctcacaagcggga	192		
Db 3888	TTGACAAACAGAGATGCTCTTACCGTGATCCGTACTGCCCCAAGCGGTTACTCCACGCG	3947		
QY 193	tcaagatcgaagccgggtgcacactctcgtgctcggcgaagtagtctgtagagcccaaggaag	252		
Db 3948	TTGCTGTGAAGCGGGATTTGCTGACTACTGTGATCAAGATGTTGGCTTGACCGTCTTA	4007		
QY 253	ccatctgagatcgacaagttctgcgcgcgagttctctctcgcgcgagacatctacaagagtagc	312		
Db 4008	TGCTGCGATATACCACTTCGCGTGAATGCTGCCGCAAGACTGCTTTTGAAAGATTGC	4067		
QY 313	gcataccgttgagagacatcttgcaactgcca	346		

QY	244	aagcgaagccatgtgcatcgcacaagctcgcgcagatgctcctgcgcgcagacatctaca	303
Db	956	gcgcgcatgcacccgtagacacccacacacttaccacccggacccgcgcgtgcgcgcgcatcgc	1015
QY	304	aggagatcagcatcaccctgtgagaagatca	333
Db	1016	ccctccacgcagacaccccgagttcattcgtca	1045

```

10 RESULT
11 US-08-526-840B-17
12 : Sequence 17, Application US/08526840B
13 : Patent No. 6001564
14 : PARENTAL INFORMATION:
15 : APPLICANT: BERGERON, Michel G.
16 : APPLICANT: OUELLETTE, Marc
17 : APPLICANT: ROY, Paul H.
18 : TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
19 : TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
20 : TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
21 : TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
22 : NUMBER OF SEQUENCES: 177
23 : CORRESPONDENCE ADDRESSES:
24 : ADDRESSEE: OVARLES & BRADY
25 : STREET: 411 East Wisconsin Avenue
26 : City: Milwaukee
27 : STATE: Wisconsin
28 : COUNTRY: USA
29 : ZIP: 53202-4497
30 : COMPUTER READABLE FORM:
31 : MEDIUM TYPE: Floppy disk
32 : COMPUTER: IBM PC compatible
33 : OPERATING SYSTEM: PC-DOS/MS-DOS
34 : SOFTWARE: PatentIn Release #1.0, Version #1.30
35 : CURRENT APPLICATION DATA:
36 : APPLICATION NUMBER: US/08/526,840B
37 : FILING DATE: 11-SEP-1995
38 : CLASSIFICATION: 435
39 : PRIOR APPLICATION DATA:
40 : APPLICATION NUMBER: US 08/304,732
41 : FILING DATE: 12-SEP-1994
42 : ATTORNEY/AGENT INFORMATION:
43 : NAME: BAKER, Jean C.
44 : REGISTRATION NUMBER: 35,433
45 : REFERENCE/DOCKET NUMBER: 850586.90012
46 : TELECOMMUNICATION INFORMATION:
47 : TELEPHONE: (414) 277-5000
48 : TELEFAX: (414) 277-5591
49 : INFORMATION FOR SEQ ID NO: 17:
50 : SEQUENCE CHARACTERISTICS:
51 : LENGTH: 1872 base pairs
52 : TYPE: nucleic acid
53 : STRANDEDNESS: double
54 : TOPOLOGY: linear
55 : MOLECULE TYPE: DNA (genomic)
56 : ORIGINAL SOURCE:
57 : ORGANISM: Pseudomonas aeruginosa
58 : US-08-526-840B-17

```

	Query Match	13.48;	Score 51.6;	DB 3;	Length 1872;
Best Local Similarity	47.38;		Pred. No. 4.8e-05;		
Matches 156;	Conservative	0;	Mismatches 174;	Indels 0;	Gaps 0;
OY	4	ccggacacaaagctcgatcatcttggtgttgagacggctctcgacttgatagtcggga	63		
Db	716	ccgccttccggccgctacacttgcgtgctatgcggccgacgccggatgcacatgatgcac	775		
OY	64	atgagcgccgcgcgcgcgcgaagaagaaggggaagacggttcgcgtctgcgtctcct	123		
Db	776	tgttgccgcaagagaccgacacaaagctgcgcgagatcaaatgatgcgatcgagagccgcgtccg	835		
OY	124	gggaactctttgatagcagctcgatgtagtcaagaggagagctctctccctccgcgaactca	183		

```

RESULT 11
US-09-327-487A-4
: Sequence 4, Application US/09327487A
: Patent No. 6352847
:
GENERAL INFORMATION:
: APPLICANT: MATSUKAWA, Hirokazu
: APPLICANT: OKA, Osamu
: APPLICANT: FUJITA, Tutosi
: APPLICANT: MIYAZAKI, Kentaro
: TITLE OF INVENTION: AMMONIA ELIMINATION LIQUID REAGENT
: FILE REFERENCE: 028022-013
: CURRENT APPLICATION NUMBER: US/09/327,487A
: PRIOR APPLICATION NUMBER: JP 10-176643
: PRIOR FILING DATE: 1998-06-09
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 4
:
LENGTH: 1284
:
TYPE: DNA
:
ORGANISM: Thermus aquaticus
:
FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(1284)
US-09-327-487A-4

```

Query Match	11.4%;	Score 44;	DB 4;	Length 1284;
Best Local Similarity	46.4%;	Pred. No. 0.0047;		
Matches 143;	Conservative	0;	Mismatches 165;	Indels
				Gaps 0;
Qy	3	accggcaccacaagcttgacatcatctgtgttggcaccgcgtctcagagcttgagatactcguygc	62	
Db	973	atcgccccccggggcccaactcaactcaagaaguygacagcgctctttagggccaccacc	1032	
Qy	63	aatgcgcccgaagagctgagagagagagagcgllcccgctgtctcgttctctcc	122	
Db	1033	ggcaccgcggccccaagtlacgtctgcccagagcaaaagtggaaccacagagctcaatctctcc	1092	
Qy	123	tgggaactcttctgattgagcagctcgaaatgagtaaaaggagagctctccctcgccagctc	182	
Db	1093	ggggagagatgattctctcgtaaccttggcctcgaaagagcgcgcggaactcatcatacaagggcc	1152	
Qy	183	acaagagagatcagatcgtgaagcgcggtcccaactcttcggtcgtcgagaaagtlacgtcggagcc	242	
Db	1153	atggagagagacatcatagacaaagggccttgcctcaactacgaactccacacgcctctctgtggcc	1212	
Qy	243	caaggcaagggccatctgagcatcgacacagttcgccgagatgtctctcgcggagagactaac	302	
Db	1213	gagggcaagcccgccacagctctcttaagaccagcgagttctgcccagggccttgatccaaagc	1272	
Qy	303	aagagata	310	
Db	1273	atgagata	1280	

RESULT 12


```

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4195 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 20..3916
US-08-340-011-1

```

```

Query Match      10.7%; Score 41.2; DB 1; Length 4195;
Best Local Similarity 46.3%; Pred. No. 0.039;
Matches 136; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

```

```

QY 51 gagatcgaggcaatggtcgccgacgactgaagaaagggaagacggtccgctgctc 110
   || || || || || || || || || || || || || || || || || || || ||
Db 2075 GACCTCCTGCTGACGACGAGCGACTCGCTGAGATGCAGTGTGGTGCCGAGCGCAC 2134
QY 111 tcgttcgtctctccttggaactctttgatgacagtcgagatgacaaaggagcgtcc 170
   || || || || || || || || || || || || || || || || || || || ||
Db 2135 GCGCCGACGATCGTGTGTACAAAGACGAGAGCTGTGAGGAAAGTGTGAGTGCAC 2194
QY 171 cctgcgacgtcacagcgagatcagcatcgagccgggtccactctcggtgctgcagaag 230
   || || || || || || || || || || || || || || || || || || || ||
Db 2195 TTGGCGGACTCTCAACCGAAGCTGAGCATCCACGCGTGGCGAGAGATGCGGAGCGC 2254
QY 231 taagtcggagcccaaggcaaggccatggtgcatcagaagttcggtcggtgctctctgc 290
   || || || || || || || || || || || || || || || || || || || ||
Db 2255 TATCTGTGACGCGTGTGCAACGCGCAAGGCGTGTGCTCACTCTCCGCCAGCGTGGCTG 2314
QY 291 gggacgatctacaaggagtagcgatcacccgtggagagcatcattgcaactgcc 344
   || || || || || || || || || || || || || || || || || || || ||
Db 2315 GAAGCTCCGAGGATTAAGGCGACATGAGATCGTGTGCTGTGCTGATCCGCGC 2368

```

RESULT 15

```

US-08-901-710-1
; Sequence 1, Application US/08901710
; Patent No. 6107046

```

GENERAL INFORMATION:

```

; APPLICANT: Alltalo, Kari
; APPLICANT: Aprelikova, Olga
; APPLICANT: Pajusola, Katri
; APPLICANT: Armstrong, Elin
; APPLICANT: Korhonen, Jaana
; APPLICANT: Kaipainen, Arja
; APPLICANT: Matikainen, Marja-Terttu
; TITLE OF INVENTION: FLU4, A RECEPTOR TYROSINE KINASE, AND USES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402

```

COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/901,710
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/340,011
; FILING DATE: 14-NOV-1994
; PRIOR APPLICATION DATA:

```

```

; APPLICATION NUMBER: 08/257,754
; FILING DATE: 09-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959,951
; FILING DATE: 09-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28113/33824
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4195 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 20..3916
US-08-901-710-1

```

```

Query Match      10.7%; Score 41.2; DB 3; Length 4195;
Best Local Similarity 46.3%; Pred. No. 0.039;
Matches 136; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

```

```

QY 51 gagatcgaggcaatggtcgccgacgactgaagaaagggaagacggtccgctgctc 110
   || || || || || || || || || || || || || || || || || || || ||
Db 2075 GACCTCCTGCTGACGACGAGCGACTCGCTGAGATGCAGTGTGGTGCCGAGCGCAC 2134
QY 111 tcgttcgtctctccttggaactctttgatgacagtcgagatgacaaaggagcgtcc 170
   || || || || || || || || || || || || || || || || || || || ||
Db 2135 GCGCCGACGATCGTGTGTACAAAGACGAGAGCTGTGAGGAAAGTGTGAGTGCAC 2194
QY 171 cctgcgacgtcacagcgagatcagcatcgagccgggtccactctcggtgctgcagaag 230
   || || || || || || || || || || || || || || || || || || || ||
Db 2195 TTGGCGGACTCTCAACCGAAGCTGAGCATCCACGCGTGGCGAGAGATGCGGAGCGC 2254
QY 231 taagtcggagcccaaggcaaggccatggtgcatcagaagttcggtcggtgctctctgc 290
   || || || || || || || || || || || || || || || || || || || ||
Db 2255 TATCTGTGACGCGTGTGCAACGCGCAAGGCGTGTGCTCACTCTCCGCCAGCGTGGCTG 2314
QY 291 gggacgatctacaaggagtagcgatcacccgtggagagcatcattgcaactgcc 344
   || || || || || || || || || || || || || || || || || || || ||
Db 2315 GAAGCTCCGAGGATTAAGGCGACATGAGATCGTGTGCTGTGCTGATCCGCGC 2368

```

```

Search completed: July 3, 2002, 08:11:38
Job time: 25863 sec

```


GenCore version 4.5
Copyright (c) 1993 - 2000 Compen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 3, 2002, 05:14:46 ; Search time 5254.53 Seconds
(without alignments)
1051.399 Million cell updates/sec

Title: US-09-300-482-569

Perfect score: 264
1 ctgactgcagcaattccca.....gacatgcttcatacttta 264

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
------------	-------	-------	-------	--------	----	----	-------------

1	51.2	19.4	7218	6	166494	166494 Sequence 14
2	41.8	15.8	197284	9	CNS01DWL	AL137230 Human chr
3	38.4	14.5	156062	2	AC097255	AC097255 Rattus no
4	38.2	14.5	1552	8	ST095923	U95923 Solanum tub
5	38.2	14.5	15313	2	AC101327	AC101327 Mus muscu
6	38.2	14.5	146741	2	AC011452	AC011452 Homo sapi
7	38.2	14.5	168230	2	AC010624	AC010624 Homo sapi
8	38.2	14.5	175999	2	AC021154	AC021154 Homo sapi
9	38.2	14.4	175602	2	AC106542	AC106542 Rattus no
10	37.6	14.2	167254	2	CNS05TDS	AL357093 Human chr
11	37.6	14.2	167390	2	AC007263	AC007263 Homo sapi
12	37.6	14.2	200542	2	CNS01R83	AL157736 Homo sapi
13	37.6	14.2	233528	2	AC099382	AC099382 Rattus no
14	37.4	14.2	139005	2	AF286112	AF286112 Homo sapi
15	37.4	14.2	165901	2	AP003474	AP003474 Homo sapi
16	37.4	14.2	171427	9	AC021590	AC021590 Homo sapi
17	37.2	14.1	16930	2	AF294352	AF294352 Homo sapi
18	37.2	14.1	79452	2	AC016536	AC016536 Homo sapi
19	37.2	14.1	107109	2	HS03781B1	AL118522 Human DNA
20	37	14.0	158641	2	AC098454	AC098454 Rattus no
21	37	14.0	179604	2	AP002959	AP002959 Homo sapi
22	36.8	13.9	73625	2	AC108383	AL596275 Human DNA
23	36.8	13.9	139273	9	AL596275	AL596275 Human DNA
24	36.8	13.9	187999	2	AC026928	AC026928 Homo sapi
25	36.8	13.9	205504	2	AC022699	AC022699 Mus muscu
26	36.6	13.9	24721	2	HS119085	Z68163 Human DNA
27	36.6	13.9	156727	2	AL627084	AL627084 Homo sapi
28	36.6	13.9	200622	2	AL158068	AL158068 Homo sapi
29	36.4	13.8	54929	2	AC105158	AC105158 Mus muscu
30	36.4	13.8	144109	2	AC012027	AC012027 Homo sapi
31	36.4	13.8	147610	2	AC099116	AC099116 Rattus no
32	36.4	13.8	170048	2	AC089988	AC089988 Homo sapi
33	36.4	13.8	192182	2	AC094597	AC094597 Rattus no
34	36.4	13.8	195052	2	AC106707	AC106707 Homo sapi
35	36.4	13.8	212382	2	AC010936	AC010936 Homo sapi
36	36.4	13.8	215196	2	AL603705	AL603705 Mus muscu
37	36.2	13.7	28812	2	AC102623	AC102623 Mus muscu
38	36.2	13.7	62109	9	AL359984	AL359984 Human DNA
39	36	13.6	569	11	HUM015530	L30662 Human STS U
40	36	13.6	111845	2	AC097570	AC097570 Rattus no
41	36	13.6	152366	9	AL138894	AL138894 Human DNA
42	36	13.6	184092	2	AC084010	AC084010 Homo sapi
43	36	13.6	200925	2	AC009090	AC009090 Homo sapi
44	36	13.6	298166	2	AC087563	AC087563 Homo sapi
45	35.8	13.6	180261	2	AC090308	AC090308 Homo sapi

ALIGNMENTS

RESULT	1
LOCUS	166494
DEFINITION	Sequence 14 from patent US 5670367.
ACCESSION	166494
VERSION	166494.1 GI:2724471
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	1 (bases 1 to 7218)
AUTHORS	Dorner, F., Scheifflinger, F. and Falkner, F. Gunter.
TITLE	Recombinant fowlpox virus
JOURNAL	Patent: US 5670367-A 14 23-SEP-1997;
FEATURES	Location/Qualifiers
source	1..7218
BASE COUNT	1944 a 1491 c 1486 g 1929 t 368 others
ORIGIN	/organism="unknown"

Query Match 19.4%; Score 51.2; DB 6; Length 7218;
Best Local Similarity 5.5%; Pred. No. 0.00053;

	Matches	11, Conservative	128, Mismatches	61, Indels	0, Gaps	0,
Oy	15	ttcccaatgcttcggtttccaagctctcaagcacaatccactgcttccttatcagaa	74			
Db	1251	yy	1310			
Oy	75	gcgcctgcgcccgcgagatctcgcttcctccactccaactcttcctcgtctttaa	134			
Db	1311	yy	1370			
Oy	135	cacaaactaacctatcgcgttcctccgcagatccatcatcactgcctcccttbaaacctcc	194			
Db	1371	yy	1430			
Oy	195	ttacgcatcaaatgctccca	214			
Db	1431	yytctaccacaattcttctta	1450			

RESULT 2
 CENSOLDML/c
 LOCUS
 DEFINITION CENSOLDML 197284 bp DNA linear PRI 02-MAY-2001
 Human Chromosome 14 DNA sequence BAC R-944C7 of library RPc1-11
 from Chromosome 14 of Homo sapiens (Human), complete sequence.
 ACCESSION AL137230
 VERSION AL137230.3 GI:13990333
 KEYWORDS
 SOURCE HMG.
 ORGANISM human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 197284)
 AUTHORS Hellis,R., Pettit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,
 Brothier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F.,
 Levy,M., Eckenberg,R., Bruls,T., deGardinhs,V., Cruaud,C.,
 Gysapay,G., Saurin,W. and Weissbach,J.
 TITLE Sequencing of the human chromosome 14
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 197284)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (02-MAY-2001) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - web : www.genoscope.cns.fr)
 COMMENT On May 7, 2001 this sequence version replaced nt17640703

```

----- Summary Statistics -----
Assembly program: Phrap, version 2.0
Quality coverage: 6.25x in Q20 bases: sum-of-contigs

```

Overall quality chart :
Range : bases

1	-	9	:	:	1
10	-	19	:	:	15
20	-	29	:	:	194
30	-	39	:	:	4106
40	-	49	:	:	9581
50	-	59	:	:	13402
60	-	69	:	:	29712
70	-	79	:	:	62136
80	-	89	:	:	78137
90	-	99	:	:	

FEATURES	Percentage of bases with a quality value >= 40 : 99 %
source	Location/Qualifiers
	1. .197284
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/chromosome="14"
	/clone="R-944C7"
	/clone_11b="RPC1-11"
	99018. .99242
	/note="matching EMBL:AA009981
	Rdbb:RH75035
	dbSTS:STS52124
	Identified using the e-PCR software (G. Schuier)"
BASE COUNT	56391 a 41571 c 42803 g 56519 t
ORIGIN	

[illegible]

RESULT	3
AC097255	
LOCUS	
DEFINITION	AC097255 156062 bp DNA linear HTG 20-DEC-2001
ACCESSION	Rattus norvegicus clone CH230-152G23, *** SEQUENCING IN PROGRESS
VERSION	***, 67 unordered pieces.
KEYWORDS	AC097255
SOURCE	HTG; HTGS_PHASE1.
ORGANISM	GI:17973953 Norway rat. Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE	1 (bases 1 to 156062)
AUTHORS	Muzny,D.M., Adams,C., Adio-Oduola,B., Alt-osman,F.R., Allen,C., Albrooks,S.L., Amaratingue,H.C., Are,J.R., Banks,T., Barbatta,J., Benton,J., Blamee,K., Blankenburg,K., Bonnih,D., Bouck,C., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burck,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carrott,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Day-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Eernhardt,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,O., Hernandez,O., Hodgson,A., Hognes,M., Holloway,C., Hollins,B., Honsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolyvet,S., Joudan,S., Karlsson,E., Kelly,S., Khan,U., Kling,L., Kovach,J., Kovar,C., Kratovic,J., Kuresh,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,Z., LiChTange,O., Ilean,C., Liu,J., Liu,M.,

Louisegeed, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R.,
Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A.,
Martinez, E., Massey, E., Mawhney, E., McLeod, M.P., Meador, M.,
Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabhat, K.,
Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N.,
Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokkwo, S.,
Oguh, M., Okunolu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B.,
Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L.,
Quiles, M., Ren, Y., Rivers, M., Rojas, A., Rojibokan, I., Rolfe, M.,
Ruiz, S., Savary, G., Scherer, S., Scott, G., Shen, H., Shoostari, N.,
Slisdon, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H.,
Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K.,
Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, R.,
Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R.,
Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C.,
Watlington, S., Williams, G., Williamson, A., Wleczek, R., Wooden, S.,
Worley, K., Wu, C., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 156062)
Moriarty, K.C.

Submitted (13-OCT-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:17062557.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GIRI
Center clone name: CH230-152G23
----- Summary Statistics
Assembly program: Phrap; version 0.990329First call to
findPhrapList
Consensus quality: 109492 bases at least Q40
Consensus quality: 119842 bases at least Q30
Consensus quality: 128566 bases at least Q20
Estimated insert size: 114589; sum-of-coverage estimation
Quality coverage: 0x in Q20 bases; agarose-gel estimation
Quality coverage: 1.4x in Q20 bases; sum-of-coverage estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 67 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 6694: contig of 6694 bp in length
* 6695 6794: gap of unknown length
* 6795 13118: contig of 6324 bp in length
* 13119 13218: gap of unknown length
* 13219 16527: contig of 3309 bp in length
* 16528 16627: gap of unknown length
* 16628 21815: contig of 5188 bp in length
* 21816 21915: gap of unknown length
* 21916 26857: contig of 4942 bp in length
* 26858 26957: gap of unknown length
* 26958 31436: contig of 4479 bp in length
* 31437 31536: gap of unknown length
* 31537 35430: contig of 3894 bp in length
* 35431 35530: gap of unknown length
* 35531 37687: contig of 2157 bp in length
* 37688 37787: gap of unknown length
* 37788 41604: contig of 3817 bp in length
* 41605 41704: gap of unknown length

41705 44844: contig of 3140 bp in length
* 44845 44944: gap of unknown length
* 44945 48135: contig of 3191 bp in length
* 48136 48235: gap of unknown length
* 48236 51261: contig of 3025 bp in length
* 51261 51361: gap of unknown length
* 51361 54250: contig of 2890 bp in length
* 54251 54350: gap of unknown length
* 54351 57355: contig of 3005 bp in length
* 57356 57455: gap of unknown length
* 57456 59485: contig of 2030 bp in length
* 59486 59585: gap of unknown length
* 59586 62310: contig of 2725 bp in length
* 62311 62410: gap of unknown length
* 62411 65496: contig of 3086 bp in length
* 65497 65596: gap of unknown length
* 65597 68251: contig of 2655 bp in length
* 68252 68351: gap of unknown length
* 68352 71491: contig of 3140 bp in length
* 71492 71591: gap of unknown length
* 71592 72701: contig of 1110 bp in length
* 72702 72801: gap of unknown length
* 72802 74689: contig of 1888 bp in length
* 74690 74789: gap of unknown length
* 74790 77463: contig of 2674 bp in length
* 77464 77563: gap of unknown length
* 77564 79838: contig of 2275 bp in length
* 79839 79938: gap of unknown length
* 79939 82456: contig of 2518 bp in length
* 82457 82556: gap of unknown length
* 82557 84625: contig of 2069 bp in length
* 84626 84725: gap of unknown length
* 84726 86114: contig of 1389 bp in length
* 86115 86214: gap of unknown length
* 86215 89234: contig of 3020 bp in length
* 89235 89334: gap of unknown length
* 89335 91946: contig of 2614 bp in length
* 91949 92048: gap of unknown length
* 92049 94209: contig of 2161 bp in length
* 94210 94309: gap of unknown length
* 94310 95901: contig of 1592 bp in length
* 95902 96001: gap of unknown length
* 96002 97710: contig of 1709 bp in length
* 97711 97810: gap of unknown length
* 97811 99597: contig of 1787 bp in length
* 99598 99697: gap of unknown length
* 99698 102001: contig of 2304 bp in length
* 102002 102101: gap of unknown length
* 102102 104337: contig of 2236 bp in length
* 104338 104437: gap of unknown length
* 104438 105784: contig of 1347 bp in length
* 105785 105884: gap of unknown length
* 105885 107825: contig of 1941 bp in length
* 107826 107925: gap of unknown length
* 107926 109144: contig of 1219 bp in length
* 109145 109244: gap of unknown length
* 109245 111225: contig of 1981 bp in length
* 111226 111326: gap of unknown length
* 111326 113568: contig of 2243 bp in length
* 113569 113668: gap of unknown length
* 113669 115302: contig of 1634 bp in length
* 115303 115403: gap of unknown length
* 115403 117409: contig of 2007 bp in length
* 117410 117509: gap of unknown length
* 117510 118595: contig of 1086 bp in length
* 118596 118695: gap of unknown length
* 118696 119789: contig of 1094 bp in length
* 119790 119889: gap of unknown length
* 119890 121183: contig of 1294 bp in length
* 121184 121283: gap of unknown length
* 121284 123106: contig of 1823 bp in length
* 123107 123206: gap of unknown length
* 123207 124316: contig of 1110 bp in length

Center: Whitehead Institute/ MIT Center for Genome Research

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS 1 (bases 1 to 168230)
TITLE DOE Joint Genome Institute.
JOURNAL Sequencing of Human Chromosome 19
REFERENCE Unpublished
AUTHORS 2 (bases 1 to 168230)
JOURNAL DOE Joint Genome Institute.
COMMENT Submitted (16-SEP-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Apr 20, 2001 this sequence version replaced gi:10305118.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 676032, BC641056
Center clone name: CITB-H1_2126E3

Summary Statistics
Consensus quality: 157703 bases at least Q40
Consensus quality: 158807 bases at least Q30
Consensus quality: 159325 bases at least Q20
Estimated insert size: 212000; agarose-1p estimation
Estimated insert size: 167230; sum-of-contrigs estimation
Quality coverage: 20.6 in Q20 bases; agarose-1p estimation
Quality coverage: 26.12 in Q20 bases; sum-of-contrigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1320: contig of 1320 bp in length
* 1321 1420: gap of unknown length
* 1421 2699: contig of 1279 bp in length
* 2700 2799: gap of unknown length
* 2800 4032: contig of 1233 bp in length
* 4033 4132: gap of unknown length
* 4133 5235: contig of 1103 bp in length
* 5236 5335: gap of unknown length
* 5336 6560: contig of 1225 bp in length
* 6561 6660: gap of unknown length
* 6661 7822: contig of 1162 bp in length
* 7823 7922: gap of unknown length
* 7923 14198: contig of 6276 bp in length
* 14199 14298: gap of unknown length
* 14299 37401: contig of 23103 bp in length
* 37402 37502: gap of unknown length
* 37503 65312: contig of 27811 bp in length
* 65313 65412: gap of unknown length
* 65413 87970: contig of 22558 bp in length
* 87971 88070: gap of unknown length
* 88071 168230: contig of 80160 bp in length.
Location/Qualifiers
1. 168230
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
/clone="CPD-2126E3"
/clone_11p="Caltech human BAC library D"

BASE COUNT 44157 a 40597 c 40066 g 42401 t 1009 others
ORIGIN

Query Match 14.5%; Score 38.2; DB 2; Length 168230;
Best Local Similarly 61.6%; Pred. No. 1.3;
Matches 61; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
4 97 gctccctcaactcaactctctccatgcgtttaatacaacaactatccgctt 156

Db 102437 GCCTCTTCCCATGAGGCTTCTCCACCCCTGTATATAAAGCAATATACCGGG 102378
Qy 157 cctccgatcatctacgcgcctcttaacctct 195
Db 102377 CCTCCCTATCCCTTCTCCATATCTTAATACTGCCT 102339

RESULT 8
AC021154 175999 bp DNA linear HTG 17-AUG-2000
LOCUS Homo sapiens chromosome 19 clone RP11-510116, WORKING DRAFT
DEFINITION
SEQUENCE, 19 unordered pieces.
ACCESSION
AC021154
VERSION AC021154.5 GI:9838241
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens
ORGANISM

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS 1 (bases 1 to 175999)
TITLE Waterston, R. H.
JOURNAL The sequence of Homo sapiens clone
REFERENCE Unpublished
AUTHORS 2 (bases 1 to 175999)
TITLE Waterston, R. H.
JOURNAL Direct Submission
COMMENT Submitted (14-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Aug 17, 2000 this sequence version replaced gi:8570265.

COMMENT

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0510116
----- Summary Statistics -----
Sequencing vector: M13; 78%
Chemistry: Dye-primer ET; 78% of reads
Chemistry: Dye-terminator Big Dye; 22% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 165027 bases at least Q40
Consensus quality: 168606 bases at least Q30
Consensus quality: 170831 bases at least Q20
Insert size: 188000; agarose-1p
Insert size: 175690; sum-of-contrigs
Quality coverage: 3.68 in Q20 bases; agarose-1p
Quality coverage: 3.97 in Q20 bases; sum-of-contrigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1820: contig of 1820 bp in length
* 1821 1920: gap of unknown length
* 1921 4432: contig of 2512 bp in length
* 4433 4532: gap of unknown length
* 4533 6992: contig of 2460 bp in length
* 6993 7092: gap of unknown length
* 7093 10867: gap of unknown length
* 10868 10967: contig of 3775 bp in length
* 10968 14067: contig of 3100 bp in length
* 14068 14167: gap of unknown length
* 14168 18869: contig of 4702 bp in length
* 18870 18870: gap of unknown length
* 18970 24630: contig of 5661 bp in length

* 24631 24730: gap of unknown length
* 24731 31836: contig of 7106 bp in length
* 31837 31936: gap of unknown length
* 31937 39296: contig of 7360 bp in length
* 39297 39396: gap of unknown length
* 39397 45890: contig of 6494 bp in length
* 45891 45990: gap of unknown length
* 45991 56324: contig of 10234 bp in length
* 56325 56324: gap of unknown length
* 56325 64404: contig of 8080 bp in length
* 64405 64504: gap of unknown length
* 64505 72478: contig of 7974 bp in length
* 72479 72578: gap of unknown length
* 72579 79599: contig of 7381 bp in length
* 79600 80059: gap of unknown length
* 80060 91688: contig of 11629 bp in length
* 91689 91788: gap of unknown length
* 91789 104423: contig of 12635 bp in length
* 104424 104523: gap of unknown length
* 104524 123430: contig of 18907 bp in length
* 123431 123530: gap of unknown length
* 123531 149278: contig of 25748 bp in length
* 149279 149378: gap of unknown length
* 149379 175999: contig of 26621 bp in length.

FEATURES
source location/Qualifiers

1. .175999 "Homo sapiens"
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/chromosome="19"
/clone="RP11-510116"
misc_feature 1.1820
/note="assembly_name:Contig6"
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misc_feature 4533.6992
/note="assembly_name:Contig8"
misc_feature 7093.10867
/note="assembly_name:Contig9"
misc_feature 10968.14067
/note="assembly_name:Contig10"
misc_feature 14168.18869
/note="assembly_name:Contig11"
misc_feature 18970.24630
/note="assembly_name:Contig12"
misc_feature 24731.31836
/note="assembly_name:Contig13"
misc_feature 31937.39296
/note="assembly_name:Contig14"
misc_feature 39397.45890
/note="assembly_name:Contig15"
misc_feature 45991.56324
/note="assembly_name:Contig16"
misc_feature 56325.64404
/note="assembly_name:Contig17"
misc_feature 64505.72478
/note="assembly_name:Contig18"
misc_feature 72579.79599
/note="assembly_name:Contig19"
misc_feature 80060.91688
/note="assembly_name:Contig20"
misc_feature 91789.104423
/note="assembly_name:Contig21"
misc_feature 104524.123430
/note="assembly_name:Contig22"
misc_feature 123531.149278
/note="assembly_name:Contig23"
misc_feature 149379.175999
/note="assembly_name:Contig24"
vector_side:left
clone_end:SP6

BASE COUNT 44579 a 42975 c 43982 g 42635 t 1828 others
ORIGIN

Query Match 14.5%: Score 38.2: DB 2: Length 175999;
Best Local Similarity 61.6%: Pred. No. 1.3;
Matches 61: Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 97 gccctccaccttaaacctctccatcgcttttaacaaacaaactatccgctt 156
Db 137920 gcccttctccatgaagcctctccaccctcgtatmaaaagacaaataccctggg 137979
Qy 157 cccctgcacatccatcgctccctccttaaacctcct 195
Db 137980 cctcccttacccttccctccatattccttaactgacct 138018

RESULT 9
AC106542/c
LOCUS
DEFINITION
AC106542 175602 bp DNA linear HTG 12-JAN-2002
Rattus norvegicus clone CH230-91P1, *** SEQUENCING IN PROGRESS ***
61 unordered pieces.
AC106542
VERSION
KEYWORDS
HTG; HTGS; PHASE1.
SOURCE
ORGANISM
Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE AUTHORS

1 (bases 1 to 175602)
Muzny,D.N., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alshrooks,S.L., Amaralunga,H.C., Are,J.R., Banks,T., Barbarta,J.,
Benton,J., Blinze,K., Blankenburg,K., Bonlath,D., Bouck,J.,
Bowle,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P., Bunay,C.,
Burck,P., Burrell,C., Burrell,K.L., Byrd,N.C., Carion,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyne,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,D.,
Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunatane,P., Hale,S.,
Hamilton,K., Harris,C., Harris,K., Hart,M., Havlik,P., Hawes,A.,
Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,
Hollins,B., Homs,J.F., Howard,S., Huber,J., Huiyk,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., Kling,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Licharge,O., Lieu,C., Liu,D., Liu,W.,
Louisege,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapa,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhney,E., Meleod,M.P., Meador,M.,
Mel,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabac,K.,
Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nockenwo,S.,
Oguy,M., Okunou,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojuboakan,I., Rolfe,M.,
Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shoshitari,N.,
Stinson,I., Sodergren,E., Sonalke,T., Sparks,A., Stanley,H.,
Stone,H., Sutton,A., Svatek,A., Tabor,T., Tamerisa,K., Tamerisa,K.,
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalob,B., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Watlington,S., Williams,G., Williams,A., Wleczyk,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gbbs,R.

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (12-JAN-2002) Human Genome Sequencing Center, Department
Direct Submission
Worley,K.C.
2 (bases 1 to 175602)
Unpublished
Direct Submission

COMMENT

of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GLIB

Center clone name: CH230-91P1

----- Summary Statistics

Assembly program: Phrap; version 0.990329First call to
findHreplst

Consensus quality: 150917 bases at least Q40

Consensus quality: 158026 bases at least Q30

Consensus quality: 164737 bases at least Q20

Estimated insert size: 150665; sum-of-coverage estimation

Quality coverage: 0x in Q20 bases; agarose-ip estimation

Quality coverage: 2.4x in Q20 bases; sum-of-coverage estimation

* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 61 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 8244: contig of 8244 bp in length

* 8245 8344: gap of unknown length

* 8345 14013: contig of 3669 bp in length

* 14014 14113: gap of unknown length

* 14114 18063: contig of 3950 bp in length

* 18064 18163: gap of unknown length

* 18164 22920: contig of 4757 bp in length

* 22921 23020: gap of unknown length

* 23021 27998: contig of 4978 bp in length

* 27999 28099: gap of unknown length

* 28099 34626: contig of 6528 bp in length

* 34627 34726: gap of unknown length

* 34727 41062: contig of 6336 bp in length

* 41063 41162: gap of unknown length

* 41163 45112: contig of 3950 bp in length

* 45113 45212: gap of unknown length

* 45213 50721: contig of 5509 bp in length

* 50722 50821: gap of unknown length

* 50822 55943: contig of 5122 bp in length

* 55944 56043: gap of unknown length

* 56044 59414: contig of 3371 bp in length

* 59415 59514: gap of unknown length

* 59515 62979: contig of 3465 bp in length

* 62980 63079: gap of unknown length

* 63080 67194: contig of 4115 bp in length

* 67195 67294: gap of unknown length

* 67295 70427: contig of 3133 bp in length

* 70428 70527: gap of unknown length

* 70528 73739: contig of 3212 bp in length

* 73740 73839: gap of unknown length

* 73840 78179: contig of 4340 bp in length

* 78180 78279: gap of unknown length

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* 95530 95629: gap of unknown length

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* 98012 101900: contig of 3869 bp in length

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* 105754 105853: gap of unknown length

* 105854 109203: contig of 3349 bp in length

* 109204 109302: gap of unknown length

* 109303 112783: contig of 3481 bp in length

* 112784 112883: gap of unknown length

* 112884 116644: contig of 3761 bp in length

* 116645 116745: gap of unknown length

* 116746 118406: contig of 1662 bp in length

* 118407 118507: gap of unknown length

* 118508 121212: contig of 2706 bp in length

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* 123134 124459: contig of 3147 bp in length

* 124460 124559: gap of unknown length

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* 126608 126707: gap of unknown length

* 126708 128164: contig of 2457 bp in length

* 128165 129165: gap of unknown length

* 129166 129264: gap of unknown length

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* 131729 133292: contig of 1564 bp in length

* 133293 133393: gap of unknown length

* 133394 134786: contig of 1394 bp in length

* 134787 134887: gap of unknown length

* 134888 136549: contig of 1663 bp in length

* 136550 136650: gap of unknown length

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* 138273 138372: gap of unknown length

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* 139459 139558: gap of unknown length

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* 143877 144923: contig of 1047 bp in length

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* 145024 146165: contig of 1142 bp in length

* 146166 146265: gap of unknown length

* 146266 147462: contig of 1137 bp in length

* 147463 147562: gap of unknown length

* 147563 149380: contig of 1818 bp in length

* 149381 149480: gap of unknown length

* 149481 150621: contig of 1141 bp in length

* 150622 150721: gap of unknown length

* 150722 152401: contig of 1680 bp in length

* 152402 152501: gap of unknown length

* 152502 154239: contig of 1738 bp in length

* 154240 154339: gap of unknown length

* 154340 155388: contig of 1249 bp in length

* 155389 155689: gap of unknown length

* 155690 156801: contig of 1113 bp in length

* 156802 156901: gap of unknown length

* 156902 158250: contig of 1349 bp in length

* 158251 158350: gap of unknown length

* 158351 159522: contig of 1172 bp in length

* 159523 159622: gap of unknown length

* 159623 160717: contig of 1095 bp in length

* 160718 160817: gap of unknown length

* 160818 162530: contig of 1713 bp in length

* 162531 162630: gap of unknown length

* 162631 164499: contig of 1869 bp in length

* 164500 164599: gap of unknown length

* 164600 166124: contig of 1525 bp in length

* 166125 166224: gap of unknown length

* 166225 167248: contig of 1024 bp in length

* 167249 167348: gap of unknown length

* 167349 168555: contig of 1307 bp in length

* 168556 168755: gap of unknown length

* 168756 169814: contig of 1059 bp in length

Query Match
Best local Similarity

14.4% Score 38; DB 2; Length 175602;
53.3% Pred. No. 1.5.

[illegible]

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 RHdb:RH42088
 RHdb:RH31324
 dbSTS:STS12299
 Identified using the e-PCR software (G. Schuler)"
 61232. .61410
 /note="matching EMBL:R01198
 RHdb:RH99189
 dbSTS:STS68937
 Identified using the e-PCR software (G. Schuler)"
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 dbSTS:STS47646
 Identified using the e-PCR software (G. Schuler)"
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 dbSTS:STS37980
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 dbSTS:STS24267
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 155206. .155317
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 dbSTS:STS53887
 Identified using the e-PCR software (G. Schuler)"
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Query Match 14.2%: Score 37.6; DB 9; Length 167254;
 Best Local Similarity 59.3%: Pred. No.1.9;
 Matches 64; Conservative 0; Mismatches 44; Indels 0; Gaps 0

Oy 76 cagctgcgccccagagattcgcgttcgcgcatcgaacattcctccatcgctttatc 135
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 Db 10169 TCTCTCCCTGTCCTTCCTCCCTCCCTCCCTCCCTTCCTTCCTTCCTC 10216

RESULT 11
 LOCUS AC007263 167390 bp DNA linear PRI 15-DEC-1999
 DEFINITION Homo sapiens chromosome 14 clone RP11-79J20 containing gene for
 checkpoint suppressor 1 (CHES1) gene, partial cds, complete
 sequence.
 AC007263
 ACCESSION AC007263.4 GI:6579248
 VERSION
 KEYWORDS
 SOURCE HTG.
 ORGANISM human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 167390)
 Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradarani,L., Birditt,B.,
 Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G.,
 James,R., Kaur,A., Madan,A., Owen,M.P., Ratcliffe,A., Shaffer,T.
 and Hood,L.
 TITLE Sequencing of human chromosome 14
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 167390)
 AUTHORS Rowen,L., Madan,A., Qin,S., Abbasi,N., Dors,M., Dickhoff,R., James,R., Loretz,C., Lasky,S., Madan,A., Prescott,S., Ratcliffe,A., Shaffer,T. and Hood,L.
 TITLE Direct Submission
 JOURNAL Submitted (08-APR-1999) Multimegabase Sequencing Center, University of Washington, PO BOX 357730, Seattle, WA 98195, USA
 REFERENCE 3 (bases 1 to 167390)
 AUTHORS Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradaran,L., Birdtlt,B., Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G., James,R., Kaur,A., Madan,A., Owen,M.P., Ratcliffe,A., Shaffer,T. and Hood,L.
 TITLE Direct Submission
 JOURNAL Submitted (15-DEC-1999) Multimegabase Sequencing Center, University of Washington, PO BOX 357730, Seattle, WA 98195, USA
 COMMENT On Dec 15, 1999 this sequence version replaced gi:4885690.
 ----- Genome Center
 Center: Multimegabase Sequencing Center
 Web site: http://chroma.mbt.washington.edu/msg_www
 Contact: leerowen@u.washington.edu
 ----- Summary Statistics
 Sequencing vector: pUC18; 108752
 Chemistry: Dye-terminator Big Dye; 90% of reads
 Assembly program: Phrap; version 0.990399

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 /map="14q31"
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 32010..32190
 /note="low quality data"
 33800..34070
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 33915..>99451
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 /note="checkpoint suppressor 1; Matches U68723 and several ESTs. The 5' UTR goes from 33915-34074 based on EST A133423. The 5'UTR of U68723 is not in this sequence.
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 ORIGIN
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 Best Local Similarity 59.3%; Pred. No. 1.9;
 Matches 64; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
 76 cgcctgcgccagatctcgcctcctcaactcctcctcgccttcaatc 135

Db 89650 CTCTTCCTCCCTCCCTCCCTCCATCCTTCCCTCCCTCCCTCCCTCTTTTACC 89709
 QY 136 acaaacctacacatccgctccctccgagatcactcgtccctc 183
 Db 89710 TCTCTCCGCTCTCTCTCTCCCTCCCTCCCTTCCCTTCTCTCTC 89757
 RESULT 12
 CDS1RG3
 LOCUS DEFINITION
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 PROGRESS ***; 2 ordered pieces.
 ACCESSION AL157736
 VERSION AL157736.3 GI:10279652
 KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 200542)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (20-SEP-2000) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 On Sep 22, 2000 this sequence version replaced gi:9212407.
 ----- Genome Center
 Center: Genoscope / Centre National de Sequencage
 Web site: http://www.genoscope.cns.fr/
 Contact: seqref@genoscope.cns.fr

 IMPORTANT: This sequence is unfinished and does not necessarily
 represent the correct sequence. Work on the sequence is in progress
 and the release of this data is based on the understanding that the
 sequence may change as work continue. The sequence may be
 contaminated with foreign sequence from E.coli, yeast, vector,
 phage, etc. . . even if efforts are made to eliminate these
 contaminating sequences. The following BAC sequence is oriented
 from the T7 to the SP6 end.
 Upstream BAC (overlapping the T7 end) : R-33N16
 Downstream BAC (overlapping the SP6 end) : R-356K23 Contigs
 Composition :
 97511 bp contig from 1 to 97511
 102931 bp contig from 97612 to 200542

 Overall quality chart :
 Range : Bases
 0 - 9 : 141
 1 - 9 : 1506
 10 - 19 : 4137
 20 - 29 : 9801
 30 - 39 : 20690
 40 - 49 : 19461
 50 - 59 : 27004
 60 - 69 : 43578
 70 - 79 : 47915
 80 - 89 : 18485
 90 - 99 : 5724

 Percentage of bases with a quality value >= 40 : 81 %.
 * NOTE: This is a "working draft" sequence. It currently
 * consists of 2 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submitor.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 97511: contig of 97511 bp in length
 * 97512 97611: gap of 100 bp

[illegible]

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

Jacobson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jollivet, S.,
 Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvath, J.,
 Kovari, C., Kratovic, U., Kuresh, A., Landry, N., Leal, B., Lewis, L. C.,
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 Weinstein, G. and Gibbs, R.

Direct Submission
 Unpublished
 2 (bases 1 to 233528)
 Worley, K.C.

Direct Submission
 Submitted (10-Nov-2001) Human genome sequencing center, Department
 of Molecular and Human genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

On Dec 21, 2001 this sequence version replaced gi:17062954.

COMMENT

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----- Genome Center
Center : Baylor College of Medicine
Center code : BCM
Web site : http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GUTP
Center clone name: CH230-69114
----- Summary Statistics
Assembly program: Phrap; version 0.990329Pfirst call to
findphraplist

Consensus quality: 222841 bases at least Q40
Consensus quality: 224953 bases at least Q30
Consensus quality: 226508 bases at least Q20
Estimated insert size: 224352; sum-of-configs estimation
Quality coverage: 0x in Q20 bases; agarose-gel estimation
Quality coverage: 5.7x in Q20 bases; sum-of-configs estimation
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 20 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
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* 27123: contig of 27123 bp in length
* 27124 27223: gap of unknown length
* 27224 56657: contig of 29434 bp in length
* 56658 56757: gap of unknown length
* 56758 86690: contig of 29933 bp in length
* 86691 86790: gap of unknown length
* 86791 109359: contig of 22569 bp in length
* 109360 109459: gap of unknown length
* 109460 126882: contig of 17423 bp in length
* 126883 142142: gap of unknown length
* 142143 142242: gap of unknown length
* 142243 154308: contig of 12066 bp in length
* 154309 154408: gap of unknown length

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OY	92	tctgtcgtctccaccattcaaacctcttcaccttcacagtctttaataacaactaatcattc	151			
Dd	52188	TTTGTTGTCTCTTCTCTCTCTCTCTTCCTCTTCTCTTCTCTCTCTCTCTCTCTCTCTTA	52129			
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	complete sequence.					
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	VERSION	AP003474.2 GI:16267361				
	KEYWORDS					
	SOURCE	Homo sapiens cell_line:FLEB 14 - 14 DNA, clone_lib:Keio BAC library clone:KB1942A3. Homo sapiens				
	ORGANISM	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
	REFERENCE	1 (bases 1 to 165901) Shimizu N, and Asakawa S, Homo sapiens DNA chromosome 8 SEQUENCE Published Only In Database (2001) In press 2 (bases 1 to 165901) Shimizu N and Asakawa S, Direct Submission Submitted (03-APR-2001) Nobuyoshi Shimizu, Keio University, School of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo 160-8582, Japan (E-mail:nshimizudm.med.keio.ac.jp, Tel.:81-3-3351-2370, Fax:81-3-3351-2370)				
	COMMENT	On Oct 18, 2001 this sequence version replaced gi:13646615.				
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 3, 2002, 07:58:10 ; Search time 796.36 Seconds

(without alignments)
569.171 Million cell updates/sec

Title: US-09-300-482-569

Perfect score: 264
Sequence: 1 ctgactgcagcaattccca.....gacatgctcatgacttta 264

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	34.8	13.2	7329	22	AAS46674	Tumour suppressor
2	34.8	13.2	107820	22	AAD16230	Human ATP-binding
3	34	12.9	27082	22	AAT70447	Human immune/haema
4	33.2	12.6	5647	24	ABL33567	Human immune syste
5	33.2	12.6	5647	24	AAS61321	Human gene regulat
6	33.2	12.6	6531	24	ABL32640	Human immune syste
7	33	12.3	9007	22	AAS46615	Tumour suppressor
8	32.6	12.3	5942	24	AAS61134	Human gene regulat
9	32.4	12.3	857	20	AAS37401	Rat U3 gene trap d

C 10	32.4	12.3	14032	24	ABL33453	Human immune syste
C 11	32	12.1	7038	22	AAS45495	Chemically pretrea
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C 15	31.8	12.0	8649	22	AAS46330	Tumour suppressor
C 16	31.6	12.0	460	22	AAS39053	Novel human diagno
C 17	31.6	12.0	16748	22	AAS65193	Human immune/haema
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C 25	31.2	11.8	53577	19	AAT94108	Human PKD1 locus b
C 26	30.8	11.7	675	24	AAS62171	Porcine muscular s
C 27	30.8	11.7	10286	22	AAS45308	Chemically pretrea
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C 40	30.2	11.4	6656	24	ABL33400	Human immune syste
C 41	30.2	11.4	8212	24	ABL99884	Mouse ischaemic co
C 42	30.2	11.4	15714	22	AAS36855	Human cardiovascular
C 43	30	11.4	6310	24	AAS61269	Human gene regulat
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ALIGNMENTS

RESULT 1	
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AC	AAS46674;
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XX	18-DEC-2001 (first entry)
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DE	Tumour suppressor gene derived chemically modified sequence #396.
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KM	Human: tumour suppressor gene; oncogene; antitumour; cytostatic;
KW	cancer; tumour; Cdc dinucleotide; single-nucleotide polymorphism; SNP;
KW	cytosine methylation; ds.
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OS	Homo sapiens.
XX	
PN	MO200168912-A2.
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PD	20-SEP-2001.
XX	
PF	15-MAR-2001; 2001MO-EP02955.
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PR	15-MAR-2000; 2000DE-1013847.
PR	06-APR-2000; 2000DE-1019058.
PR	07-APR-2000; 2000DE-1019173.
PR	30-JUN-2000; 2000DE-1032529.
PR	01-SEP-2000; 2000DE-1043826.
XX	
PA	(EPIC-) EPIGENOMICS AG.
PI	Olek A, Piepenbrock C, Berlin K;
XX	

DR WPI: 2001-602752/68.

XX Fragments of chemically modified genes associated with tumour suppressor
PT genes and oncogenes, useful in designing primers and probes for
PT analysing diseases associated with cytosine methylation state e.g.
cancer

PS Claim 1; SEQ ID No 396; 27pp; English.

XX
CC The invention relates to a nucleic acid comprising a sequence of 18
CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
CC bisulphite, of genes associated with tumour suppression and
CC oncogenes having a sequence taken from 536 (actually 533 since
CC numbers 408, 458 and 500 are missing from the sequence listing) sequences
CC (53) and sequences complementary to (53). The nucleic acid may be a
CC peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may
CC form part of a set of probes for detecting the cytosine methylation state
CC and/or single nucleotide polymorphisms and also to be used in an
CC array for analysing diseases associated with CpG dinucleotides e.g.
CC cancers and tumours. The probes can also be used in a method for
CC ascertaining genetic and/or epigenetic parameters for the diagnosis
CC and/or therapy of existing diseases or the predisposition to specific
CC diseases, by analysing cytosine methylations. The parameters may be
CC compared to another set of genetic and/or epigenetic parameters, the
CC differences serving as basis for diagnosis and/or prognosis events which
CC are disadvantageous to patients. The present sequence is one of the
CC 533 genomic sequences derived from tumour suppressor genes and
CC oncogenes. Sequences with even numbered Seq ID numbers are the
CC complementary sequence of the corresponding odd numbered sequence (e.g.
CC ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence
CC is missing).

CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 7329 BP; 1917 A; 141 C; 1597 G; 3670 T; 4 other;

Query Match 13.2%; Score 34.8; DB 22; Length 7329;
Best Local Similarity 50.6%; Pred. No. 0.45;

Matches 84; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

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Oy 152 cgcttcctccgcatcattcactcgctcctctctaaacctccta 197
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RESULT 2

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ID AAD16230 standard; DNA: 107820 BP.

XX AAD16230;

XX 19-NOV-2001 (first entry)

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KW Human: prenatal diagnosis; dermal lesion; cardiovascular disease: MRP6;
KW Multidrug Resistance-associated protein 6; macular degeneration: ABCG6;
KW ATP-binding cassette transporter; arterial insufficiency; chromosome 16;
KW Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
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XX Homo sapiens.

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RESULT 3
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 KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cytostatic; gene therapy; vaccine; metastasis; ds.
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 OS Homo sapiens.
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 PN W0200157182-A2.

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PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
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PA (EPIC-) EPIGENOMICS AG.
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PI Olek A, Piepenbrock C, Berlin K;
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DR WPI: 2001-602752/68.
XX
PT Fragments of chemically modified genes associated with tumour suppressor
PT genes and oncogenes, useful in designing primers and probes for
PT analysing diseases associated with cytosine methylation state e.g.
cancer
XX
XX
PS Claim 1; SEQ ID No 337; 27pp; English.
XX
CC The invention relates to a nucleic acid comprising a sequence of 18
CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
CC bisulphite, of genes associated with tumour suppression and
CC oncogenes having a sequence taken from 536 (actually 533 since
CC numbers 408, 458 and 500 are missing from the sequence listing) sequences
CC (ss) and sequences complementary to (ss). The nucleic acid may be a
CC peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may
CC form part of a set of probes for detecting the cytosine methylation state
CC and/or single nucleotide polymorphisms and also to be used in an
CC array for analysing diseases associated with CpG dinucleotides e.g.
CC cancers and tumours. The probes can also be used in a method for
CC ascertaining genetic and/or epigenetic parameters for the diagnosis
CC and/or therapy of existing diseases or the predisposition to specific
CC diseases, by analysing cytosine methylations. The parameters may be
CC compared to another set of genetic and/or epigenetic parameters, the
CC differences serving as basis for diagnosis and/or prognosis events which
CC are disadvantageous to patients. The present sequence is one of the
CC 533 genomic sequences derived from tumour suppressor genes and
CC oncogenes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
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KW Human; Gene regulation-associated gene; severe combined immunodeficiency;
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KW asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome;
KW renal disease; Preecclampsia; cardiac allograft vascular disease;
KW colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour;
KW immunostimulant; cardiac; anti-inflammatory; coagulant; antithrombotic;
KW nephrologic; gynecological; anti-tumour; immunosuppressive; cytostatic.
OS
XX Homo sapiens.
XX
XX WO20017375-A2.
XX
PD 18-Oct-2001.
XX
XX
XX 06-APR-2001; 2001WO-EP03968.
XX
XX
PR 06-APR-2000; 2000DE-1019058.
PR 07-APR-2000; 2000DE-1019173.
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
XX (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI: 2002-017470/02.
XX
XX
PT New nucleic acid sequences from chemically modified genes associated
PT with gene regulation, useful for analysing cytosine methylations for
PT diagnosis and therapy of diseases e.g. severe combined immunodeficiency
PT disease
XX
XX
XX Claim 1; SEQ ID No 91; 26pp; English.
XX
CC The invention relates to 224 nucleic acid sequences comprising at least
CC 18 bases of a chemically pretreated gene associated with gene regulation
CC selected from 43 known genes (or complementary sequences). The
CC chemical pretreatment converts cytosine bases unmethylated at the
CC 5-position to uracil or another base with hybridisation behaviour
CC dissimilar to cytosine, to enable analysis of cytosine methylations.
CC The DNA sequences, oligomers (or sets/arrays) and method are
CC useful in the diagnosis of diseases (or predisposition to diseases)
CC associated with gene regulation and in therapy of such diseases, by
CC enabling analysis of the cytosine methylation patterns of such genes,
CC kits are provided. They are especially useful in diagnosis
CC and therapy of e.g. severe combined immunodeficiency disease, cardiac
CC disorders, haemophilia, solid tumours and cancer, Werner syndrome,
CC asthma, HDR syndrome, Saethre-Chotzen syndrome, renal disease,
CC preecclampsia, graft versus-host disease. The present sequence is a
CC sequence included in the sequence data for this specification and is
CC associated with the human gene regulation-associated genes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 5942 BP; 1401 A; 180 C; 1593 G; 2768 T; 0 other;
Query Match 12.3%; Score 32.6; DB 24; Length 5942;
Best Local Similarity 58.0%; Pred. No. 2.2;
Matches 76; Conservative 0; Mismatches 54; Indels 1; Gaps 1;
QY 86 ccgagatctcgcctccacactcaaacctctccatcgcttcaacacaaactaa 145
DB 4876 CCGGACACTCTCTCCAGCTTCCTTAATCCCGAGCAGCAGCTTACTACCAAAAAACATA 4817
QY 146 cctatcgcctccctccagcatcactcgcctcccttaaacactcctcagatcaa 205
DB 4816 CCTATCTCTCGACCAATCGCTAAATC-CTTATTAAGCTTTAAACCCCTAATAGCATCA 4758
QY 206 atgctcccaaa 216

Db 4757 TCCGCCCAAAA 4747

RESULT 9

AA57401/C
ID AA57401 standard; DNA; 857 BP.

AC AA57401;

DT 24-JUL-1999 (first entry)

DE Rat U3 gene trap derived nucleic acid 14A13E-RE.

KW Gene trap; rat; cellular gene; viral infection; cell survival; cancer;

KW tumour progression; suppression; identification; viral growth;

KW tumour suppressor; prevention; screening; therapeutic agent; ss.

OS Rattus norvegicus.

PN WO9919481-A2.

PD 22-APR-1999.

PF 08-OCT-1998; 98WO-US21276.

PR 10-OCT-1997; 97US-0062021.

PA (UYVA-) UNIV VANDERBILT.

PI Dubois RN, Organ EL, Rubin DH;

DR WPI; 1999-326546/27.

PT Nucleic acid encoding tumor suppressors and products required for
PT viral infection

PS Claim 1; Page 58-59; 94pp; English.

CC This invention describes novel rat-derived nucleic acid fragments from
CC cellular genes that are necessary for viral infection but not for cell
CC survival, or that suppress tumor progression. The products of the
CC invention (AA57371-X57497) can be used in methods of identifying
CC cellular genes necessary for viral growth and cellular genes that
CC function as tumour suppressors and for reducing or preventing such
CC infections or cancer. They may also be used in screening for potential
CC therapeutic agents. These sequences can be targeted without significant
CC side effects (contrast targeting genes essential for viral growth).

SO Sequence 857 BP; 189 A; 151 C; 234 G; 220 T; 63 other;

Query Match 12.3%; Score 32.4; DB 20; Length 857;
Best Local Similarity 47.5%; Pred. No. 1.2;

Matches 66; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

OY 62 ttccattatagaagcgttcgcccgcagatctcgcttcctcaactcaactcttc 121

Db 248 TTGCGATATAGAACTNCANTCTTTCCANGTCTGTTCCCAACCCNTACAAAGCTCNC 189

OY 122 catcgcttataacacaaactaactacgttcgcttcctccgcatcattcctgcctcc 181

Db 188 TTTTCCGTTTGGCNCACCTCCCAACANTTTCCCTTANTCCGCCGACCCGTTGTCNC 129

OY 182 tcttaaacctcctcaagg 200

Db 128 NCCTGGAATTTTTCGCG 110

RESULT 10

ABL33453/C
ID ABL33453 standard; DNA; 14032 BP.

AC ABL33453;

XX 26-MAR-2002 (first entry)

DE Human immune system associated gene SEQ ID NO: 1426.

KW Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antianaemic; cytosolic; noctropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antiporiatic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW gene; ds.

OS Homo sapiens.

PN WO200200928-A2.

PD 03-JAN-2002.

PF 02-JUL-2001; 2001WO-EP07537.

PR 30-JUN-2000; 2000DE-1032529.

PR 01-SEP-2000; 2000DE-1043826.

PA (EPIC-) EPIGENOMICS AG.

PI Olek A, Plepenbrock C, Berlin K;

DR WPI; 2002-130909/17.

PT Nucleic acid comprising fragment of chemically modified gene, useful
PT for diagnosis and treatment of diseases associated with abnormal
PT cytosine methylation

PS Claim 1; SEQ ID NO 1426; 32pp + Sequence Listing; German.

CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention.

SO Sequence 14032 BP; 3389 A; 291 C; 3605 G; 6747 T; 0 other;

Query Match 12.3%; Score 32.4; DB 24; Length 14032;
Best Local Similarity 60.0%; Pred. No. 3.6;

Matches 54; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

OY 106 ctctcaaaccttcttcacgtcttataacacaaactaactacgttcctcccgat 165

Db 7580 CCTTAATTCACCACTTAACCCCTTTTAAAAATTAACATAACCACTAAT 7521

OY 166 ccaatcactgcctccctcttaaacctcct 195

Db 7520 AATATATATATCTCTCTAATTAACATACT 7491

RESULT 11

AA545495/C
ID AA545495 standard; DNA; 7038 BP.

AC AA545495;

DT 18-DEC-2001 (first entry)

DE Chemically pretreated complementary DNA associated with cell cycle #100.

XX Cell cycle; human; CPG dinucleotide; cytosine methylation; HIV; aging;

KW	human immunodeficiency virus; neurodegenerative disorder; solid tumour;
KV	griif-versus-host disease; glomerular disease; Lewy body disease; cancer;
KM	arthritis; arteriosclerosis; anti-HIV, neuroprotective; antiallathritic;
KW	Immunosuppressive; antitumour; cytosolic; antiarteriosclerotic; ds;
KM	PCR primer.
XX	
OS	Homo sapiens.
XX	
PN	WO200168911-A2.
XX	
PD	20-SEP-2001.
XX	
PF	15-MAR-2001; 2001WO-EP02945.
XX	
PR	15-MAR-2000; 2000DE-1013847.
PR	06-APR-2000; 2000DE-1013058.
PR	07-APR-2000; 2000DE-1019173.
PR	30-JUN-2000; 2000DE-1033529.
PR	01-SEP-2000; 2000DE-1043826.
XX	
PA	(EPIC-) EPIGENOMICS AG.
XX	
P1	Olek A, Plepenbrock C, Berlin K;
DR	WPI; 2001-602751/68.
XX	
PT	Designing primers and probes for analysing diseases associated with
PT	cytosine methylation state e.g. arthritis, cancer, aging,
PT	arteriosclerosis comprising fragments of chemically modified genes
XX	
PT	associated with cell cycle -
PS	Claim 1; SEQ ID No 200; 28pp; English.
CC	
XX	
CC	Sequences AA545326-AA545520 represent chemically pretreated genomic DNA
CC	molecules associated with the cell cycle and specific PCR primers of the
CC	invention. The sequences are useful for detecting the methylation state
CC	of all CpG dinucleotides in a sequence and therefore for analysing
CC	associated diseases. By analysing cytosine methylations in the pretreated
CC	DNA, genetic and/or epigenetic parameters for the diagnosis and therapy
CC	of existing diseases or the predisposition to specific diseases can be
CC	ascertained. The parameters may be compared to another set of genetic
CC	and/or epigenetic parameters, the differences serving as basis for
CC	diagnosis and/or prognosis events which are disadvantageous to patients.
CC	The sequences of the invention are useful for the diagnosis and therapy
CC	of HIV infection, neurodegenerative disorders, graft-versus-host disease,
CC	aging, glomerular disease, Lewy body disease, arthritis,
CC	arteriosclerosis, solid tumours and cancers.
SQ	
SQ	Sequence 7038 BP; 1390 A; 375 C; 2162 G; 3111 T; 0 other;

[illegible]

XX
DE
vV

Murine apoptosis related DNA sequence #199.

KW Apoptosis; mouse; cancer; autoimmune disease; viral infection;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
 KW reperfusion injury; stroke; liver damage; dilatory cardiomyopathy;
 KW transgenic animal; hepatotropic; antialcoholism; cyclostatic;
 KW immunosuppressive; virulence; nootropic; neuroprotective; vasotropic;
 KW antiParkinsonian; cerebroprotective; ds.
 XX Mus sp.
 XX Mus sp.

Mus sp.

PN DE10126344-A1.

PD 24-JAN-2002.

PF 30-MAY-2001; 2001DE-1026344.

PR 14-JUL-2000; 2000DE-1034303.

PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
VY

PI Grimm S, Schoenfeld N, Brazilius E, Cramer U, Gewies A, Voss F:
PI Mund T, ...

Pl Mund T, Albayrak T, Gille H, Klein M, xx

DR WPI; 2002-115563/16.

PT New apoptosis-associated nucleic acid sequences and polypeptides, PT useful for diagnosis, treatment and prevention of e.g. tumors and PT neurodegeneration -

PS Claim 1; Page 214-215; 227pp; German.

The present invention relates to nucleic acids from the mouse, where the nucleic acid is associated with apoptosis. The sequences can be used in the diagnosis, treatment and prevention of diseases associated with excessive or inadequate apoptosis, including tumours, autoimmune diseases, viral infections, degenerative diseases (Alzheimer's, Parkinson's and Huntington's diseases), reperfusion injury, stroke and alcohol-induced injury to the liver, for identifying agents for treating these diseases, and to prepare transgenic animals in which expression of an apoptosis related sequence is altered. These are useful for genetic and/or pharmacological investigations of apoptosis and related diseases, including dilatory cardiomyopathy. The present sequence is one of the apoptosis related sequences of the invention.

Sequence 1684 BP; 147 A; 669 C; 52 G; 459 T; 357 other;

Query Match	12.0%	Score 31.8;	DB 24;	Length 1684;
Best Local Similarity	43.7%	Prod No 3		

Matches	69;	Conservative	0;	Mismatches	87.
---------	-----	--------------	----	------------	-----

[illegible]

RESULT 14

ABL32262/c
ID ABL32262 standard; DNA; 5565 BP.

AC ABL32262;

DT 26-MAR-2002 (first entry)

XX Human immune system associated gene SEQ ID NO: 235.
DE
XY

KM Human immune system disease; cytosine methylation; antislathmatic;
KM antiarteriosclerotic; antinematocystostatic; neotropic;
KM neuroprotective; anti-HIV; anticyanotic; ophthalmological;
KM antirheumatic; antiarthritis; antidiabetic; antiparasitic;
KM antinflammatory; cancer; eye disease; antileukemia; anemia;
KM acute myeloid leukemia; Alzheimer's disease; AIDS; epilepsy;
KM neurofibromatosis; rheumatoid arthritis; psoriasis; glaucoma;
KM gene; ds.

OS Homo sapiens.

PN W0200200928-A2

PD 03-JAN-2002

02-JUL-2001; 2001WO-EP07537.

PR 30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1032529

PR 01-SEP-2000; 2000DE-1043826.
XX

PA (EPiG-) EPIGENOMICS AG
xx

Olek A, Piepenbrock C, Berlin K;

DR WPI; 2002-130909/17.
xx

PT Nucleic acid comprising fragment of chemically modified gene, useful
PT for diagnosis and treatment of diseases associated with abnormal
PT cytosine methylation -

PS Claim 1; SEQ ID NO 235; 32pp + Sequence Listing; German

The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.

sequence 5565 BP; 1405 A; 76 C; 1326 G; 2758 T; 0 other,

Query Match	12.08;	Score 31.8;	DB 24;	Length 5565;
Best Local Similarity	52.7%;	Pred No. 4;		

Matches	69;	Conservative	0;	Mismatches	62;	Indels	0;	Gaps	0
---------	-----	--------------	----	------------	-----	--------	----	------	---

QY	67	tatcagaagcgtctgcgccccgagatctcgctgtcccaactcaaacctcttccatcg	120
Db	403	TATAAAAATTCCTACTGCCACTATATGCCACCTCTTCACTATATTCCTTTCTACCAA	344
QY	127	ctttaatcacacaactaactatcgcgtctccctcgcgatccatccaactcgcctccctta	180
Db	343	CCCTACTGATATTCACATATAAATTTCTTCCACCAACTCTCCCAAAAACATTAACCTTCCAA	288
QY	187	aaactccctta	197
Db	283	AAACCTCACTA	273

RESULT 15

AAS46330/c
ID AAS46330 standard; DNA: 8649 BP.

AC AAS46330;

DT 18-DEC-2001 (first entry)

Tumour suppressor gene derived chemically modified sequence #52

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 3, 2002, 08:11:38 ; Search time 185.98 Seconds
(without alignments)
348.679 Million cell updates/sec

Title: US-09-300-482-569

Perfect score: 264
1 ctgactgtcagcagatcccca.....gacatgctcagatctta 264

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_NA: *
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq: *
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq: *
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5: /cgn2_6/ptodata/2/ina/PTUS.COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51.2	19.4	7218	1 US-08-232-463-14	Sequence 14, Appl
2	31.4	11.9	4002	3 US-09-356-952-9	Sequence 9, Appl
3	31.2	11.8	53526	3 US-08-658-136-2	Sequence 2, Appl
4	31.2	11.8	53577	3 US-08-658-136-1	Sequence 1, Appl
5	30.6	11.6	289	4 US-09-007-005-17	Sequence 17, Appl
6	30.6	11.6	289	4 US-09-244-796-17	Sequence 17, Appl
7	29.2	11.1	12793	4 US-09-004-838-124	Sequence 124, App
8	29	11.0	5751	4 US-09-417-455-7	Sequence 7, Appl
9	29	11.0	5751	4 US-09-348-942-7	Sequence 7, Appl
10	28.8	10.9	2575	1 US-08-135-511-33	Sequence 33, Appl
11	28.8	10.9	2575	1 US-08-483-852-10	Sequence 10, Appl
12	28.8	10.9	2575	1 US-08-361-458-5	Sequence 5, Appl
13	28.8	10.9	2575	1 US-08-477-953-10	Sequence 10, Appl
14	28.8	10.9	2575	1 US-08-187-453-33	Sequence 33, Appl
15	28.8	10.9	2575	2 US-08-477-952-10	Sequence 10, Appl
16	28.8	10.9	36741	4 US-09-301-665-3	Sequence 3, Appl
17	28.6	10.8	433	4 US-08-905-223-261	Sequence 261, App
18	27.8	10.5	248	4 US-09-007-005-32	Sequence 32, Appl
19	27.8	10.5	248	4 US-09-244-796-32	Sequence 32, Appl
20	27.8	10.5	277	4 US-09-007-005-3	Sequence 3, Appl
21	27.8	10.5	277	4 US-09-244-796-3	Sequence 3, Appl
22	27.8	10.5	614	4 US-09-328-111-212	Sequence 212, App
23	27.6	10.5	273	4 US-09-004-838-138	Sequence 138, App
24	27.6	10.5	2035	4 US-08-960-780-10	Sequence 10, Appl
25	27.6	10.5	2035	4 US-09-073-898-10	Sequence 10, Appl
26	27.6	10.5	3131	3 US-09-035-648-23	Sequence 23, Appl
27	27.6	10.5	3131	4 US-09-001-951-23	Sequence 23, Appl

C 28	27.6	10.5	3562	4 US-09-360-197-1	Sequence 1, Appl
C 29	27.6	10.5	3647	4 US-09-360-197-7	Sequence 7, Appl
C 30	27.6	10.5	18443	4 US-09-078-294-6	Sequence 6, Appl
C 31	27.4	10.4	420	4 US-09-328-111-413	Sequence 413, App
C 32	27.4	10.4	681	4 US-09-299-378-1	Sequence 1, Appl
C 33	27	10.2	933	6 5340934-12	Patent No. 5340934
34	27	10.2	2444	2 US-08-821-355A-2	Sequence 2, Appl
35	27	10.2	2444	3 US-09-003-687A-2	Sequence 2, Appl
36	27	10.2	2444	3 US-09-136-605-2	Sequence 2, Appl
37	27	10.2	11495	4 US-09-056-105-9	Sequence 38, Appl
38	26.8	10.2	1255	1 US-08-518-878B-38	Sequence 38, Appl
39	26.8	10.2	1255	1 US-08-294-522B-38	Sequence 38, Appl
40	26.8	10.2	1255	2 US-08-470-868A-38	Sequence 38, Appl
41	26.8	10.2	1545	1 US-08-400-275-17	Sequence 17, Appl
42	26.8	10.2	1596	2 US-08-807-861A-38	Sequence 38, Appl
43	26.8	10.2	1596	3 US-09-210-681-38	Sequence 38, Appl
44	26.8	10.2	1596	3 US-08-946-719A-38	Sequence 38, Appl
45	26.8	10.2	2125	4 US-09-303-639-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-232-463-14
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEFFLINGER, F.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300,6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZgpt-Fls
US-08-232-463-14

```

? RESULT 2
? US-09-356-952-9
? Sequence 9, Application US/09356952
? Patent No. 611/663
? GENERAL INFORMATION:
? APPLICANT: Borlack-Sjodin, Ann
? APPLICANT: Margarit, S. M.
? APPLICANT: Bor-Sogl, Daina
? APPLICANT: Cole, Philip
? APPLICANT: Kuriyan, John
? TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
? FILE REFERENCE: 600-1-1228N
? CURRENT APPLICATION NUMBER: US/09/356,952
? CURRENT FILING DATE: 1999-07-19
? EARLIER APPLICATION NUMBER: 60/093,631
? EARLIER FILING DATE: 1998-07-21
? NUMBER OF SEQ ID NOS: 14
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 9
? LENGTH: 4002
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-09-356-952-9

```

[illegible]

RESULT 3
 US-08-658-136-2
 Sequence 2, Application US/08658136
 Patent No. 6071717
 GENERAL INFORMATION:
 APPLICANT: KLINGER, KATHERINE W
 APPLICANT: LANDES, GREGORY M
 APPLICANT: BORN, TIMOTHY C
 APPLICANT: CONNORS, TIMOTHY D
 APPLICANT: DACKOWSKI, WILLIAM
 APPLICANT: GERMINO, GREGORY
 APPLICANT: OTAN, PENG
 TITLE OF INVENTION: POLYCLYTIC KIDNEY DISEASE GENE

```

1 NUMBER OF SEQUENCES: 58
2 CORRESPONDENCE ADDRESS:
3 ADDRESSEE: GENZYME CORPORATION
4 STREET: ONE MOUNTAIN ROAD
5 CITY: FRAMINGHAM
6 STATE: MASSACHUSETTS
7 COUNTRY: USA
8 ZIP: 01701
9
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: FLOPPY disk
12 COMPUTER: IBM PC compatible
13 OPERATING SYSTEM: PC-DOS/MS-DOS
14 SOFTWARE: Patentln Release #1.0, Version #1.25
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/08/658,136
17 FILING DATE:
18
19 CLASSIFICATION: 435
20 ATTORNEY/AGENT INFORMATION:
21 NAME: LASSEN, ELIZABETH
22 REGISTRATION NUMBER: 31,845
23 REFERENCE/DOCKET NUMBER: GEN4-17.8
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: 508-872-8400
26 TELEFAX: 508-872-5415
27 INFORMATION FOR SEQ. ID NO: 2:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 53526 base pairs
30 TYPE: nucleic acid
31 STRANDEDNESS: single
32 TOPOLOGY: linear
33
34 MOLECULE TYPE: DNA (genomic)
35
36 US-08-658-136-2

```

Query Match	11.8%	Score 31.2	DB 3	Length 53526
Best Local Similarity	47.4%	Pred. No. 1.2	Mismatches 103	Indels 0
Matches	93	Conservative	0	Gaps 0
QY 18	cgaatggcttcggtttccaaagcftcaagaagcaaatccactgtctctatcagaagc	77		
DB 35274	CCCATGGCCCTCTCTCCCTCCCTCCATCCCTCTCTCCCTCCCTCCCTCCATCC	35333		
QY 78	cttggcccccggagattctgtctctccacettcaaaccttctccatgcgttttaacac	137		
DB 35334	ATCCCCCTCTCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	35393		
QY 138	aaaacttaacctacgcgtcttcctccgatccattcaatcgtccctctctaaacctctta	197		
DB 35334	CTCTCCCTCTCTCTCCATCCCTCTCTCCATCCCTCTCTCTCTCTCTCTCTCT	35453		
QY 198	cgagtaaatgctccc	213		
DB 35454	CCTCCCATCT	35469		

4 RESULT
 US-08-658-136-1
 : Sequence 1, Application US/08658136
 : Patent No. 6071717
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: KLINER, KATHERINE W
 : APPLICANT: LANDER, GREGORY M
 : APPLICANT: BURN, TIMOTHY C
 : APPLICANT: CONNORS, TIMOTHY D
 : APPLICANT: DACKOWSKI, WILLIAM
 : APPLICANT: GERMINO, GREGORY
 : APPLICANT: GIAN, PENG
 : TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
 :
 : NUMBER OF SEQUENCES: 58
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: GENZYME CORPORATION
 : STREET: ONE MOUNTAIN ROAD
 : CITY: FRAMINGHAM


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GENERAL INFORMATION:
APPLICANT: CHIANG, John
TITLE OF INVENTION: Cholesterol 7a-Hydroxylase Gene
TITLE OF INVENTION: Regulatory Elements and Transcription Factors
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/187,453
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/135,488
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/135,511
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/135,510
FILING DATE: 13-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 18748/188
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 2575 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-187-453-33

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; Patent No. 5851780
; GENERAL INFORMATION:
; APPLICANT: CHIANG, John Young Ling
; TITLE OF INVENTION: Genomic DNA of Human Cholesterol
; TITLE OF INVENTION: 7a-Hydroxylase and Methods of using it
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
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STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
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APPLICATION NUMBER: US/08/477,952
FILING DATE: 07-JUN-1995
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APPLICATION NUMBER: US 08/361,458
FILING DATE: 21-DEC-1994
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APPLICATION NUMBER: US 08/135,511
FILING DATE: 13-OCT-1993
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APPLICATION NUMBER: US 08/135,488
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/135,510
FILING DATE: 13-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 18748/221 HOCE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
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OM nucleic - nucleic search, using sw model

Run on: July 3, 2002, 07:58:30 ; Search time 796.36 Seconds

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Listing first 45 summaries

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SUMMARIES

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7	34	11.3	579	23	AAAS4595
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11	32.4	10.8	543	18	AAV75242	Staphylococcus aur
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20	30.6	10.2	1051	19	AAV27386	Streptococcus pneu
21	30.6	10.2	13206	19	AAV52166	Staphylococcus pneu
22	30.6	10.2	22243	18	AAV74475	Staphylococcus pneu
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ALIGNMENTS

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KW	Protein identification; signal transduction pathway;	
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OS	Arabidopsis thaliana.	
PN	EP1033405-A2.	
XX	06-SEP-2000.	
PD	25-FEB-2000; 2000EP-0301439.	
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PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0148368.
PR 17-AUG-1999; 99US-0148175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 30-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159283.
PR 13-OCT-1999; 99US-0159284.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.

PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145129.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 26-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145291.
PR 27-JUL-1999; 99US-0145918.
PR 28-JUL-1999; 99US-0145919.
PR 02-AUG-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0146389.
PR 04-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 05-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147182.
PR 06-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 09-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 23-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158602.
PR 08-OCT-1999; 99US-0158623.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.

PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159337.
PR 18-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 12.0%; Score 36; DB 21; Length 2614;
Best Local Similarity 48.5%; Pred. No. 0.21;
Matches 99; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 1 gattattgacaacaccctctgttgatgtgacatcaaatgtcctaactgacctg 60
|| | ||| | | | ||| ||| | | | ||| |
Db 667 gccatccctgagatcttcgagactcctggaattggaattcaactacacgcctcttggacaag 726
QY 61 aacttgcaactcctctgtaattgtcaatttcaagagcgagacacctaaccgca 120
| | | | | | | | | | | | | | | | | | | |
Db 727 gatcgcctaattgtctgtttagctctgtcgtggaagcatttgcctgcagattcaaca 766
QY 121 atggtctactgaagtaagaaagccttcagagatggggctgcaattctgaaacag 180
| | | | | | | | | | | | | | | | | | | |
Db 787 aacctgagctgaaagtaagtaagcaccactacacatatgcgattccttggaatgtgtcaga 846
QY 181 gctgtgcaattactcaagaanaatt 204
| | | | | | | | | | | | | | | | | | | |
Db 847 tggaggtatcttctaataagacgtt 870

RESULT 5

ID ABL17694 standard; DNA; 3436 BP.

XX ABL17694;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 4555.

KW Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical; gene; ds.

OS Drosophila melanogaster.

PN W0200171042-A2.

XX 27-SEP-2001.

PF 23-MAR-2001; 2001WC-US09231.

PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX

PA (PEKE) PE CORP NY.
PI Venter JC, Adams M, Li PWD, Myers EW;
PI WPI: 2001-656860/75.
XX
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX
PS Claim 1: SEQ ID NO 4555; 21bp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC (AB57737-AB572072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 3436 BP; 836 A; 970 C; 681 G; 949 T; 0 other;

Query Match 11.5%; Score 34.6; DB 23; Length 3436;
Best Local Similarity 49.2%; Pred. No. 0.65;
Matches 91; Conservative 0; Mismatches 94; Indels 0; Gaps 0;
OY 94 agagcgaggagcaacctgaaccgcaatgctctactagaaglacagaagcctcaag 153
DB 3099 ATAGCATTTGGAATCATTCACCTGCTATTTTATAGCCGGAATACMAAGCTTTCTGTG 3040
OY 154 atgcgaggctgcaatctcgaacaaggggtgcaattactcaagaanaattctcgttg 213
DB 3039 ATACGATTTATGCTATTCATTGAGGCTTTTATTTACTAAGATAAATTTTAAATA 2980
OY 214 ataacactgctagaatagaaggatgtagctcggttctcctagtgttgatggtgtg 273
DB 2979 GCTGCGCTTACAAATAATAGATCATATATCATCTGGGTTTTTAACTCGTAGTGTGCGG 2920
OY 274 gtagg 278
DB 2919 CGAGG 2915

RESULT 6
AB123418/C
ID AB123418 standard; DNA; 4605 BP.
XX
XX
XX ABL23418;
AC
XX
XX 26-MAR-2002 (first entry)
DT
XX
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 21727.
DE
XX
XX Drosophila: developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
XX Drosophila melanogaster.
OS
XX
XX WO200171042-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
XX 23-MAR-2001; 2001WO-US09231.
PF
XX
XX 23-MAR-2000; 2000US-191637P.
PR
XX
XX 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE) PE CORP NY.

XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI: 2001-656860/75.
XX
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX
PS Claim 1: SEQ ID NO 21727; 21bp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC (AB57737-AB572072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 4605 BP; 1222 A; 787 C; 1319 G; 1277 T; 0 other;

Query Match 11.5%; Score 34.6; DB 23; Length 4605;
Best Local Similarity 49.2%; Pred. No. 0.73;
Matches 91; Conservative 0; Mismatches 94; Indels 0; Gaps 0;
OY 94 agagcgaggagcaacctgaaccgcaatgctctactagaaglacagaagcctcaag 153
DB 534 ATAGCATTTGGAATCATTCACCTGCTATTTTATAGCCGGAATACMAAGCTTTCTGTG 475
OY 154 atgcgaggctgcaatctcgaacaaggggtgcaattactcaagaanaattctcgttg 213
DB 474 ATACGATTTATGCTATTCATTGAGGCTTTTATTTACTAAGATAAATTTTAAATA 415
OY 214 ataacactgctagaatagaaggatgtagctcggttctcctagtgttgatggtgtg 273
DB 414 GCTGCGCTTACAAATAATAGATCATATATCATCTGGGTTTTTAACTCGTAGTGTGCGG 355
OY 274 gtagg 278
DB 354 CGAGG 350

RESULT 7
AAS54595
ID AAS54595 standard; DNA; 579 BP.
XX
XX
XX AAS54595;
AC
XX
XX 13-FEB-2002 (first entry)
DT
XX
XX Staphylococcus aureus DNA for cellular proliferation protein #907.
DE
XX
XX Antisense; ds; prokaryotic cellular proliferation gene;
KW antibiotic; antibacterial; drug design.
XX
XX Staphylococcus aureus.
OS
XX
XX WO200170955-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
XX 21-MAR-2001; 2001WO-US09180.
PF
XX
XX 21-MAR-2000; 2000US-191078P.
PR
XX
XX 23-MAY-2000; 2000US-206848P.
PR
XX
XX 26-MAY-2000; 2000US-20727P.
PR
XX
XX 23-OCT-2000; 2000US-242578P.
PR
XX
XX 27-NOV-2000; 2000US-253625P.

PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
XX
XX (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
XX WPI; 2001-611495/70.
DR P-PSDB; AAU36736.
XX
XX
XX New polynucleotides for the identification and development of
XX antibiotics, comprise sequences of antisense nucleic acids -
XX
PS Claim 27; Seq ID No 8232; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
XX prokaryotic cellular proliferation, their use in identifying the
XX genes, their use in the discovery of novel antibiotics, the essential
XX genes themselves and the encoded proteins. The prokaryotes used are
XX Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
XX pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
XX invention is also useful for the identification of potential new targets
XX for antibiotic development. The antisense nucleic acid sequence can be used
XX and to obtain antibodies capable of binding to the expressed proteins,
XX The proteins can be used to screen compounds in rational drug discovery
XX programmes. The antisense nucleic acid sequence is also useful to screen
XX for homologous nucleic acids which are required for cell proliferation in
XX a wide variety of organisms. The present sequence encodes an
XX essential prokaryotic cellular proliferation protein.
XX Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic
XX format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
SQ
Sequence 579 BP; 177 A; 63 C; 114 G; 225 T; 0 other;

Query Match 11.3%; Score 34; DB 23; Length 579;
Best Local Similarity 51.3%; Pred. No. 0.51;
Matches 79; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 41 aatgtcacaactggaactggaactggaactctgttaattgttaattcctaagcg 100
DB 270 aattgtactctgtcaactagtaactaacttctgttagtaagcaatcatattatgcag 329
QY 101 aggcacacctggaacccgcgaatggtctactagaagtaagaagcctcagatgcgg 160
DB 330 agaattgcccgtactcgtttactactacaattgacaagaagattcgttaagtcgacg 389
QY 161 gctcgaattctggaacagaggtgttcgaattact 194
DB 390 tggtaaatgtataaataaacaagcagcttact 423

RESULT 8
ABL07679/c
ID ABL07679 standard; cDNA; 7178 BP.
XX
XX ABL07679;
XX
XX
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 17519.
XX
XX
XX Drosophila: developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ss.
XX
XX Drosophila melanogaster.
XX
XX WO200171042-A2.

PD 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
XX
XX 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
DR P-PSDB; ABB63576.
XX
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -
XX
PS Claim 1; Seq ID NO 17519; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABBS7737-ABR2072).
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
SQ
Sequence 7178 BP; 1928 A; 2032 C; 1807 G; 1411 T; 0 other;

Query Match 11.1%; Score 33.2; DB 23; Length 7178;
Best Local Similarity 59.6%; Pred. No. 2.5;
Matches 56; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 184 ttcgaattcaagaagaatctctgttgatgaacacgcagaaatgagatgtag 243
DB 3354 tgggattttagccacgaagacttggcattgcttgagagagagcttggtg 3295
QY 244 ctccggttccatgtttgatctggtggtgtag 277
DB 3294 ctacttttgctacttggattgggtggtgtag 3261

RESULT 9
ABL07678/c
ID ABL07678 standard; cDNA; 12400 BP.
XX
XX ABL07678;
XX
XX
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 17516.
XX
XX
XX Drosophila: developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ss.
XX
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
XX
XX 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE) PE CORP NY.

XX Polynucleotide(s) and proteins derived from *Staphylococcus aureus*
PT stored on computer readable medium and used in the production of
PT anti-S.aureus vaccines
XX

PS Claim 1; Page 1752-1753; 3271pp; English.

XX This sequence represents one of 5191 *Staphylococcus aureus* DNA sequences
CC of the invention. The DNA sequences are recorded on a computer readable
CC medium, preferably selected from a floppy or hard disk, random access
CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
CC the *S.aureus* DNA sequences allows putative functions to be assigned so
CC that protein-encoding or regulatory regions of commercial, therapeutic or
CC industrial importance can be obtained. Specifically, sequences which are
CC likely to encode antigens have been identified and these polypeptides can
CC be used in a vaccine composition against *S.aureus* infection. The
CC polypeptides can also be used in a kit for the immunodetection of
CC *S.aureus* in a sample. *S.aureus* is implicated in numerous human diseases,
CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
CC skin and surgical wound infections, scalded skin syndrome, toxic shock
CC syndrome, etc. Organisms transformed with the DNA sequences can be used
CC for recombinant production of the polypeptides. The new DNA sequences
CC (and their fragments) are useful as primers or probes for isolating
CC homologues of any of the *S.aureus* DNA sequences contained on the
CC computer readable medium.
XX

SO Sequence 543 BP; 178 A; 100 C; 53 G; 152 T; 60 other;

Query Match 10.8%; Score 32.4; DB 18; Length 543;
Best Local Similarity 50.6%; Pred. No. 1.7;
Matches 78; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

OY 41 aattgtcactagagaccctggaactctgttaattgcatcttaagaagcgg 100
DB 207 AATTGTACTTGGCAACTAGACTAGCAAAATCTGTAGTACAAATCATTTATTGCGAG 148
OY 101 aggcacacctggaaccgcgaatgctactagaagaagcctcagaagtgcgg 160
DB 147 AGAATTTGCCGTACTGGTTACTTACTCAAAATTGAACAAGGATTCGTAAGTGCAGC 88
OY 161 gctgcaattctcgaacaggggtgttgcgaattact 194
DB 87 TGGTCATTTAGTAAATTAATAAACGACGATTACT 54

RESULT 12
AAS55056

ID AAS55056 standard; DNA: 579 BP.

AC AAS55056;

DT 13-FEB-2002 (first entry)

DE *Staphylococcus aureus* DNA for cellular proliferation protein #1368.

KW Antisense; ds; prokaryotic cellular proliferation gene;
KW antibiotic; antibacterial; drug design.

OS *Staphylococcus aureus*.

WO200170955-A2.

PD 27-SEP-2001.

PF 21-MAR-2001; 2001MO-0509180.

XX 21-MAR-2000; 2000US-191078P.

PR 23-MAY-2000; 2000US-206848P.

PR 26-MAY-2000; 2000US-207727P.

PR 23-OCT-2000; 2000US-242578P.

PR 27-NOV-2000; 2000US-253625P.

PR 24-DEC-2000; 2000US-257931P.

PR 16-FEB-2001; 2001US-269308P.

XX (ELIT-) ELITRA PHARM INC.

PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawack JD, Carr GJ;
PI Yamamoto RT, Xu HH;

DR WPI: 2001-611495/70.

P-PSDB; AAU37197.

PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -

PS Claim 27; Seq ID No 8693; 511pp; English.

XX The invention relates to antisense inhibitors of genes essential to
XX prokaryotic cellular proliferation, their use in identifying the
XX genes, their use in the discovery of novel antibiotics, the essential
XX genes themselves and the encoded proteins. The prokaryotes used are
XX *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
XX *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
XX invention is also useful for the identification of potential new targets
XX for antibiotic development. The antisense nucleic acids can also be used
XX to identify proteins used in proliferation, to express these proteins,
XX and to obtain antibodies capable of binding to the expressed proteins.
XX The proteins can be used to screen compounds in rational drug discovery
XX programmes. The antisense nucleic acids which are required for cell proliferation in
XX a wide variety of organisms. The present sequence encodes an
XX essential prokaryotic cellular proliferation protein.
XX Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic
XX format directly from Wipo at
XX ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 579 BP; 176 A; 63 C; 115 G; 225 T; 0 other;

Query Match 10.8%; Score 32.4; DB 23; Length 579;
Best Local Similarity 50.6%; Pred. No. 1.7;
Matches 78; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

OY 41 aattgtcactagagaccctggaactctgttaattgcatcttaagaagcgg 100
DB 270 aattgtactgttgcaactagactaacaattctgtatgaatacattatattatgccag 329
OY 101 aggcacacctggaaccgcgaatgctactagaagaagcctcagaagtgcgg 160
DB 330 agaattgcgcgaactcgttctactactacaattgaacaagatcgtgaagtcagc 389
OY 161 gctgcaattctcgaacaggggtgttgcgaattact 194
DB 390 tgtcgaattaggttaataataaacagcagttact 423

RESULT 13
AAK82196/C

ID AAK82196 standard; DNA: 11161 BP.

AC AAK82196;

DT 07-NOV-2001 (first entry)

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37008.

KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;

KW cytostatic; gene therapy; vaccine; metastasis; ds.

OS *Homo sapiens*.

WO200157182-A2.

PN 09-AUG-2001.

XX

XX

XX

XX. 17-JAN-2001; 2001WO-US01354.
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PR 28-JUN-2000; 2000US-0214886.
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PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
XX

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AC AAK82197;

DT 07-NOV-2001 (first entry)
 XX

Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37009.

Human; immune; haematopoietic; immune/haematopoietic antigen; cancer, cytostatic; gene therapy; vaccine; metastasis; ds.

OS Homo sapiens.

PN W0200157182-A2.

PD 09-AUG-2001.

17-JAN-2001; 2001WO-US01354.

PR 31-JAN-2000; 2000US-0179065

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CC	PI	Rosen CA, Barash SC, Ruben SM;	
CC	XX		
CC	DR	WPI; 2001-483426/52.	
CC	XX		
CC	PT	Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -	
CC	PT		
CC	XX		
CC	PS	Disclosure; SEQ ID NO 37009; 3071bp + Sequence Listing; English.	
CC	XX		
CC	AA	AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For	

CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK4950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 11934 BP; 3616 A; 1963 C; 1946 G; 4409 T; 0 other;

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Qy 120	aatggcttactaagaagtaagaagaacgcttcagaagatgcggygctgtgcaattctcgaacag	179		
Db 7114	AAGGGCTCCCGAATTCCTTAAGAACATGACGGTGAATGCATTAAGAACA	7055		
Qy 180	ggctgttgcaattactcaagaa	201		
Db 7054	TCGAAATAAGATTTAAAAAAA	7033		

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AC AA013336;
XX
DT 19-MAR-1999 (first entry)
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DE Enterococcus faecalis genome contig SEQ ID NO:399.
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KM Enterococcus faecalis; contig; detection; Enterococcal infection;
KM vaccine; attenuation; computer readable medium; ds.
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OS Enterococcus faecalis.
XX
PN M09850555-A2.
XX
PD 12-NOV-1998.
XX
PF 04-MAY-1998; 98MO-US08985.
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PR 14-NOV-1997; 97US-0066009.
PR 06-MAY-1997; 97US-0044031.
PR 16-MAY-1997; 97US-0046555.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Barash SC, Dillon PJ, Kunsch CA;
XX
DR WPI; 1999-045171/04.
XX
PT New isolated Enterococcus faecalis polynucleotides and polypeptides
PT - used to develop products for the detection of Enterococcus and for
PT use in vaccines for prevention or attenuation of Enterococcus
PT infection.
XX
PS Claim 1; Page 1592-1609; 2084pp; English.
XX
CC A computer readable medium has been developed which has recorded on it
CC 982 nucleotide sequences isolated from the Enterococcus faecalis genome.

CC AAX12938 to AAX13919 represent these nucleotide sequences which are
CC primary nucleotide sequences, also known as contigs. The computer-based
CC system can identify fragments of the Enterococcus faecalis genome with
CC commercial importance. The products can be used to detect the presence
CC of Enterococcus faecalis in samples. They can also be used for
CC diagnosing Enterococcal infection in an animal and monitoring
CC progression of disease, and for identifying agents which can be used to
CC modulate the growth or pathogenicity of Enterococcus faecalis, or
CC another related organism, in vivo or in vitro. In particular the
CC polypeptides encoded by the Enterococcus faecalis nucleotide sequences
CC can be used in vaccines to prevent or attenuate an Enterococcal
CC infection.
CC
XX
SQ Sequence 32768 BP; 10797 A; 5960 C; 7083 G; 8921 T; 7 other;

Query Match 10.5%; Score 31.6; DB 20; Length 32768;
Best Local Similarity 51.4%; Pred. No. 15;
Matches 73; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
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QY 112 aaaccgcaatggtctactagaagtaagaagccctcagaagtgcgggctgcaattct 171
DB 4906 aattcatcaattcatatataagtttttgaagtgggaataacgcagacaagaacaaatca 4965
QY 172 cgaacaagggtgttgcattac 193
DB 4966 aggtcgtggtgttccatctcc 4987

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Searched: 21979536 seqs, 10817449327 residues

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41: /cgn2_6/ptodata/2/pna/US045_COMB.seq: *
42: /cgn2_6/ptodata/2/pna/US046_COMB.seq: *
43: /cgn2_6/ptodata/2/pna/US047_COMB.seq: *

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	300	100.0	300	16	US-09-237-183A-276	Sequence 276, App
2	300	100.0	300	17	US-09-300-482-619	Sequence 619, App
3	300	100.0	300	17	US-09-304-517A-10554	Sequence 10554, A
4	300	100.0	300	17	US-09-371-146A-10554	Sequence 10554, A
5	300	100.0	300	36	US-09-985-678-10554	Sequence 10554, A
6	296.8	98.9	2199	33	US-09-865-439A-11076	Sequence 11076, A
7	295.2	98.4	434	27	US-09-696-664A-7280	Sequence 7280, App
8	295.2	98.4	434	55	US-09-161-619-7119	Sequence 7119, App
9	288.8	96.3	1850	25	US-09-654-617-267132	Sequence 267132, A
10	288.8	96.3	1850	27	US-09-684-016-267132	Sequence 267132, A
11	285.6	95.2	590	33	US-09-865-419A-51737	Sequence 51737, A
12	223.8	74.6	1056	25	US-09-654-617-388605	Sequence 388605, A
13	223.8	74.6	1056	27	US-09-684-016-388605	Sequence 388605, A
14	218.4	72.8	509	32	US-09-849-529A-21745	Sequence 21745, A
15	218.4	72.8	509	58	US-09-196-868-21733	Sequence 21733, A
16	208.8	69.6	397	33	US-09-874-708A-57982	Sequence 57982, A
17	208.8	69.6	397	60	US-09-211-750-56895	Sequence 56895, A
18	208.8	69.6	1156	28	US-09-705-926-2660	Sequence 2660, App
19	208.8	69.6	1368	25	US-09-654-617-3903	Sequence 3903, App
20	208.8	69.6	1368	27	US-09-684-016-3903	Sequence 3903, App
21	208.8	69.6	2218	33	US-09-874-708A-46195	Sequence 46195, A
22	203.4	67.8	362	26	US-09-669-817A-33549	Sequence 33549, A
23	197.6	65.9	1836	28	US-09-708-427-10377	Sequence 10377, A
24	197.6	65.9	1836	35	US-09-938-842A-12322	Sequence 12322, App
25	194.8	64.9	470	25	US-09-654-617-405674	Sequence 405674, A
26	194.8	64.9	470	27	US-09-684-016-405674	Sequence 405674, A
27	194.8	64.9	470	58	US-09-197-872-53225	Sequence 53225, A
28	194.8	64.8	2413	33	US-09-867-716-19334	Sequence 19334, A
29	192.8	64.3	343	64	US-09-253-456-3653	Sequence 3653, App
30	190	63.3	593	64	US-09-253-456-28250	Sequence 28250, A
31	184	61.3	411	25	US-09-654-617-234017	Sequence 234017, A

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

```
32 184 61.3 411 26 US-09-666-355A-23565 Sequence 23565, A
33 184 61.3 411 27 US-09-684-016-234017 Sequence 234017,
34 175.4 58.5 481 33 US-09-874-708A-5054 Sequence 5054, Ap
35 175.4 58.5 481 60 US-60-211-750-4911 Sequence 4911, Ap
36 174.4 58.1 488 33 US-09-874-708A-520 Sequence 520, App
37 174.4 58.1 488 60 US-60-211-750-520 Sequence 520, App
38 159.8 53.3 235 17 US-09-300-482-628 Sequence 285, App
39 159.8 53.3 235 17 US-09-300-482-628 Sequence 285, App
40 159.8 53.3 235 17 US-09-304-517A-22437 Sequence 22437, A
41 159.8 53.3 235 17 US-09-371-146A-22437 Sequence 22437, A
42 159.8 53.3 235 36 US-09-985-678-22437 Sequence 22437, A
43 159.8 53.3 248 16 US-09-288-328A-664 Sequence 664, App
44 159.8 53.3 248 47 US-60-085-147-664 Sequence 664, App
45 145 46.3 248 16 US-09-237-183A-282 Sequence 282, App
```

ALIGNMENTS

```
RESULT 1
US-09-237-183A-276
; Sequence 276, Application US/09237183A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Fisher, Dane K.
; APPLICANT: Liu, Jindong
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
; FILE REFERENCE: 38-21(15089)B
; CURRENT APPLICATION NUMBER: US/09/237,183A
; CURRENT FILING DATE: 1999-01-26
; PRIOR APPLICATION NUMBER: US 60/067,000
; NUMBER OF SEQ ID NOS: 2814
; SEQ ID NO 276
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Zea mays
US-09-237-183A-276
```

```
Query Match 100.0%; Score 300; DB 16; Length 300;
Best Local Similarity 100.0%; Pred. No. 2.6e-87;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 gattattgaacacccgacatcctctgctggaatgatacacaattgctcaactagagactg 60
D 1 gattattgaacacacccgacatcctctgctggaatgatacacaattgctcaactagagactg 60
QY 61 aactggcaactactctctgtaattgttaattcttaagaagcgagagacacactgaaccgca 120
D 61 aactggcaactactctctgtaattgttaattcttaagaagcgagagacacactgaaccgca 120
QY 121 atggtctactagaagtaacagaagccttcagagatcgaggcgacgaattctcgaaacagg 180
D 121 atggtctactagaagtaacagaagccttcagagatcgaggcgacgaattctcgaaacagg 180
QY 181 gtgttgcaattactcaagaataattctctgttggataaactctagaaatagagggatggt 240
D 181 gtgttgcaattactcaagaataattctctgttggataaactctagaaatagagggatggt 240
QY 241 tagctcggttcctactgattgattggtggtgtagagactcagaagaatgctgctggtg 300
D 241 tagctcggttcctactgattgattggtggtgtagagactcagaagaatgctgctggtg 300
```

```
RESULT 2
US-09-300-482-619
; Sequence 619, Application US/09300482
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jindong
; APPLICANT: Peschke, Virginia M.
```

```
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
; FILE REFERENCE: 04983.0031.US01/38-21(15365)B
; CURRENT APPLICATION NUMBER: US/09/300,482
; CURRENT FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 699
; SEQ ID NO 619
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Zea mays
US-09-300-482-619
```

```
Query Match 100.0%; Score 300; DB 17; Length 300;
Best Local Similarity 100.0%; Pred. No. 2.6e-87;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 gattattgacaacaccgacatcctctgctggaatgatacacaattgctcaactagagactg 60
D 1 gattattgacaacaccgacatcctctgctggaatgatacacaattgctcaactagagactg 60
QY 61 aactggcaactactctctgtaattgttaattcttaagaagcgagagacacactgaaccgca 120
D 61 aactggcaactactctctgtaattgttaattcttaagaagcgagagacacactgaaccgca 120
QY 121 atggtctactagaagtaacagaagccttcagagatcgaggcgacgaattctcgaaacagg 180
D 121 atggtctactagaagtaacagaagccttcagagatcgaggcgacgaattctcgaaacagg 180
QY 181 ggttcgcaattctcaagaataattctctgttggataaactctgataagaaggatggt 240
D 181 ggttcgcaattctcaagaataattctctgttggataaactctgataagaaggatggt 240
QY 241 tagctcggttcctactgattgattggtggtgtagagactcagaagaatgctgctggtg 300
D 241 tagctcggttcctactgattgattggtggtgtagagactcagaagaatgctgctggtg 300
```

```
RESULT 3
US-09-304-517A-10554
; Sequence 10554, Application US/09304517A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jindong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)B
; CURRENT APPLICATION NUMBER: US/09/304,517A
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 10554
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Zea mays
US-09-304-517A-10554
```

```
Query Match 100.0%; Score 300; DB 17; Length 300;
Best Local Similarity 100.0%; Pred. No. 2.6e-87;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 gattattgacaacaccgacatcctctgctggaatgatacacaattgctcaactagagactg 60
D 1 gattattgacaacaccgacatcctctgctggaatgatacacaattgctcaactagagactg 60
QY 61 aactggcaactactctctgtaattgttaattcttaagaagcgagagacacactgaaccgca 120
D 61 aactggcaactactctctgtaattgttaattcttaagaagcgagagacacactgaaccgca 120
QY 121 atggtctactagaagtaacagaagccttcagagatcgaggcgacgaattctcgaaacagg 180
D 121 atggtctactagaagtaacagaagccttcagagatcgaggcgacgaattctcgaaacagg 180
QY 181 ggttcgcaattctcaagaataattctctgttggataaactctgataagaaggatggt 240
```

```
Db 181 ggtgtgcaattactcaagaataatctctgttgatatacaactgctacgaatagaagatggt 240
QY 241 tagctcggttccctactatgtttgattggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 300
Db 241 tagctcggttccctactatgtttgattggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 300
```

RESULT 4

```
US-09-371-146A-10554
; Sequence 10554, Application US/09371146A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jindong
; TITLE OF INVENTION: ANNOTATED PLANT GENES
; FILE REFERENCE: 38-21(15097)C
; CURRENT APPLICATION NUMBER: US/09/371,146A
; CURRENT FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 294310
; SEQ ID NO 10554
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Zea mays
US-09-371-146A-10554
```

```
Query Match 100.0%; Score 300; DB 17; Length 300;
Best Local Similarity 100.0%; Pred. No. 2.6e-87;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 gatttatgacaacaccgcatctctgctggtgattgatcatcaaatgtctcaactagacctg 60
Db 1 gatttatgacaacaccgcatctctgctggtgattgatcatcaaatgtctcaactagacctg 60
QY 61 aactggcaactactctctgtaattgtcaattcttaagaagcggaagcacactgaaaccgca 120
Db 61 aactggcaactactctctgtaattgtcaattcttaagaagcggaagcacactgaaaccgca 120
QY 121 atggtctactagaagtagaagaagccttcagagatgcggggcgctgcaattctcgaaccag 180
Db 121 atggtctactagaagtagaagaagccttcagagatgcggggcgctgcaattctcgaaccag 180
QY 181 gttgtgcaattactcaagaanaattctctgtgttgatacaactgcttagaagaagatggt 240
Db 181 gttgtgcaattactcaagaanaattctctgtgttgatacaactgcttagaagaagatggt 240
QY 241 tagctcggttccctactatgtttgattggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 300
Db 241 tagctcggttccctactatgtttgattggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 300
```

RESULT 5

```
US-09-985-678-10554
; Sequence 10554, Application US/09985678
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jindong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 16517, 255/38-21(15097)F
; CURRENT APPLICATION NUMBER: US/09/985,678
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 10554
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Zea mays
US-09-985-678-10554
```

```
Query Match 100.0%; Score 300; DB 35; Length 300;
Best Local Similarity 100.0%; Pred. No. 2.6e-87;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 gatttatgacaacaccgcatctctgctggtgattgatcatcaaatgtctcaactagacctg 60
Db 1 gatttatgacaacaccgcatctctgctggtgattgatcatcaaatgtctcaactagacctg 60
QY 61 aactggcaactactctctgtaattgtcaattcttaagaagcggaagcacactgaaaccgca 120
Db 61 aactggcaactactctctgtaattgtcaattcttaagaagcggaagcacactgaaaccgca 120
QY 121 atggtctactagaagtagaagaagccttcagagatgcggggcgctgcaattctcgaaccag 180
Db 121 atggtctactagaagtagaagaagccttcagagatgcggggcgctgcaattctcgaaccag 180
QY 181 gttgtgcaattactcaagaanaattctctgtgttgatacaactgcttagaagaagatggt 240
Db 181 gttgtgcaattactcaagaanaattctctgtgttgatacaactgcttagaagaagatggt 240
QY 241 tagctcggttccctactatgtttgattggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 300
Db 241 tagctcggttccctactatgtttgattggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 300
```

RESULT 6

```
US-09-865-439A-11076/c
; Sequence 11076, Application US/09865439A
; GENERAL INFORMATION:
; APPLICANT: Edgeton, Michael D
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(51936)B
; CURRENT APPLICATION NUMBER: US/09/865,439A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/207,458
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 119126
; SEQ ID NO 11076
; LENGTH: 2199
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3205-077-A12_FLI
US-09-865-439A-11076
```

```
Query Match 98.9%; Score 296.8; DB 33; Length 2199;
Best Local Similarity 99.3%; Pred. No. 6.6e-86;
Matches 298; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 gatttatgacaacaccgcatctctgctggtgattgatcatcaaatgtctcaactagacctg 60
Db 1420 GATTATTGACAAACACCGATCCGCTGGGATGATCATCAATTGGCTCAACATGAGGACTG 1361
QY 61 aactggcaactactctctgtaattgtcaattcttaagaagcggaagcacactgaaaccgca 120
Db 1360 AACTGGCAACTACTCTTGTATTTGTCATTCTTAAGAGCGGAGCACACTGNAACCGGA 1301
QY 121 atggtctactagaagtagaagaagccttcagagatgcggggcgctgcaattctcgaaccag 180
Db 1300 ATGGTCTACTAGAAGTAGAAGAAAGCCTTCAAGATGACAGGCTGCATCTGAAACAG 1241
QY 181 gttgtgcaattactcaagaanaattctctgtgttgatacaactgcttagaagaagatggt 240
Db 1240 GTGTTGCAATTACTCAAGAAATTCCTGTGGATTAACACTGTAAGATGAGAGGATGGT 1181
QY 241 tagctcggttccctactatgtttgattggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 300
Db 1180 TAGCTCGGTTCCATGATTGTGATTGGGTTGGTGTGATGAGACTTCAGAAATGACGCTGTG 1121
```

RESULT 7

```
US-09-664-7280
; Sequence 7280, Application US/09696664A
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Andersen, Scott E.
; APPLICANT: Dubois, Patricia
; APPLICANT: Mahadeo, Debbie A.
; APPLICANT: Masucci, James D.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(51721)B
; CURRENT APPLICATION NUMBER: US/09/696,664A
; PRIOR FILING DATE: 2000-10-25
; PRIOR FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 17472
; SEQ ID NO 7280
; LENGTH: 434
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3279-041-P1-K1-F8
US-09-696-664A-7280
```

Query Match 98.4%; Score 295.2; DB 27; Length 434;
Best Local Similarity 99.0%; Pred. No. 1,1e-85;

Matches 297; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
QY 1 gattattgacaacacgcgactctgctggatgatacacaatgctcaactaggactg 60
   |||||||
DB 100 gattattgacaacacgcgactctgctggatgatacacaatgctcaactaggactg 159
QY 61 aactggcaactactctgttaattctcttcttaagcggagacacccgaaaccgca 120
   |||||||
DB 160 aactggcaactactctgttaattctcttcttaagcggagacacccgaaaccgca 219
QY 121 atggtctactagaagtaacagaagccttcagagatgctgggctgcgaattctcgaacagg 180
   |||||||
DB 220 atggtctactagaagtaacagaagccttcagagatgctgggctgcgaattctcgaacagg 279
QY 181 gtgttgcattactacaagaataatctctgttgaatacactgctagaaatagaggatggt 240
   |||||||
DB 280 gtgttgcattactacaagaataatctctgttgaatacactgctagaaatagaggatggt 339
QY 241 tagctcggttccctatgttgaattggtggtgtagtagactcaagaatgctgctgtg 300
   |||||||
DB 340 tagctcggttccctatgttgaattggtggtgtagtagactcaagaatgctgctgtg 399
```

RESULT 8

```
US-60-161-619-7119
; Sequence 7119, Application US/60161619
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Andersen, Scott E.
; APPLICANT: Dubois, Patricia
; APPLICANT: Mahadeo, Debbie A.
; APPLICANT: Masucci, James D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(51721)A
; CURRENT APPLICATION NUMBER: US/60/161,619
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 7685
; SEQ ID NO 7119
; LENGTH: 434
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3279-041-P1-K1-F8
```

US-60-161-619-7119

Query Match 98.4%; Score 295.2; DB 55; Length 434;
Best Local Similarity 99.0%; Pred. No. 1,1e-85;

Matches 297; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
QY 1 gattattgacaacacgcgactctgctggatgatacacaatgctcaactaggactg 60
   |||||||
DB 100 gattattgacaacacgcgactctgctggatgatacacaatgctcaactaggactg 159
QY 61 aactggcaactactctgttaattctcttcttaagcggagacacccgaaaccgca 120
   |||||||
DB 160 aactggcaactactctgttaattctcttcttaagcggagacacccgaaaccgca 219
QY 121 atggtctactagaagtaacagaagccttcagagatgctgggctgcgaattctcgaacagg 180
   |||||||
DB 220 atggtctactagaagtaacagaagccttcagagatgctgggctgcgaattctcgaacagg 279
QY 181 gtgttgcattactacaagaataatctctgttgaatacactgctagaaatagaggatggt 240
   |||||||
DB 280 gtgttgcattactacaagaataatctctgttgaatacactgctagaaatagaggatggt 339
QY 241 tagctcggttccctatgttgaattggtggtgtagtagactcaagaatgctgctgtg 300
   |||||||
DB 340 tagctcggttccctatgttgaattggtggtgtagtagactcaagaatgctgctgtg 399
```

RESULT 9

```
US-09-654-617-267132
; Sequence 267132, Application US/09654617
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jindong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/654,617
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 267132
; LENGTH: 1850
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB3279-041-P1-K1-F8
US-09-654-617-267132
```

Query Match 96.3%; Score 288.8; DB 25; Length 1850;
Best Local Similarity 97.7%; Pred. No. 2,6e-83;

Matches 293; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
QY 1 gattattgacaacacgcgactctgctggatgatacacaatgctcaactaggactg 60
   |||||||
DB 430 gattattgacaacacgcgactctgctggatgatacacaatgctcaactaggactg 489
QY 61 aactggcaactactctgttaattctcttcttaagcggagacacccgaaaccgca 120
   |||||||
DB 490 aactggcaactactctgttaattctcttcttaagcggagacacccgaaaccgca 549
QY 121 atggtctactagaagtaacagaagccttcagagatgctgggctgcgaattctcgaacagg 180
   |||||||
DB 550 atggtctactagaagtaacagaagccttcagagatgctgggctgcgaattctcgaacagg 609
QY 181 gtgttgcattactacaagaataatctctgttgaatacactgctagaaatagaggatggt 240
   |||||||
DB 610 gtgttgcattactacaagaataatctctgttgaatacactgctagaaatagaggatggt 669
QY 241 tagctcggttccctatgttgaattggtggtgtagtagactcaagaatgctgctgtg 300
   |||||||
DB 670 tagctcggttccctatgttgaattggtggtgtagtagactcaagaatgctgctgtg 729
```

RESULT 10

US-09-684-016-267132

Sequence 267132, Application US/09684016
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jindong
TITLE OF INVENTION: Annotated Plant Genes
FILE REFERENCE: 38-21(15097)D
CURRENT APPLICATION NUMBER: US/09/684,016
CURRENT FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 09/654,617
PRIOR FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 463173
SEQ ID NO 267132
LENGTH: 1850
TYPE: DNA
ORGANISM: Zea mays
US-09-684-016-267132

Query Match 96.3%; Score 288.8; DB 27; Length 1850;
Best Local Similarity 97.7%; Pred. No. 2.6e-83;
Matches 293; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 gattattgacacacccgctcctgctggtatgcatcatcaattgtcactagagacctg 60
|||
Db 430 gattattgacacacccgctcctgctggtatgcatcatcaattgtcactagagacctg 489
Qy 61 aactggaactactctctgtaattgcatcttcaagaagcgagacacactgaaccgca 120
|||
Db 490 aactggaactactctctgtaattgcatcttcaagaagcgagacacactgaaccgca 549
Qy 121 atggtctactagaatgacagaagccttcagagatcggtggtcgaattctcgaacaag 180
|||
Db 550 atggtctactagaatgacagaagccttcagagatcggtggtcgaattctcgaacaag 609
Qy 181 gtgtgcaattcactcaagaanaattctctgttgatacaactgctagatagagggatgt 240
|||
Db 610 gtgtgcaattcactcaagaanaattctctgttgatacaactgctagatagagggatgt 669
Qy 241 tagctcggttccctatgtttgattggtgtgtgtgtagagacttcagaanaatgtctgtgtg 300
|||
Db 670 tagctcggttccctatgtttgattggtgtgtgtgtagagacttcagaanaatgtctgtgtg 729

RESULT 11
US-09-865-419A-51737
Sequence 51737, Application US/09865419A
GENERAL INFORMATION:
APPLICANT: Conner, Timothy W.
APPLICANT: Wu, Kunsheng
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(51935)B
CURRENT APPLICATION NUMBER: US/09/865,419A
CURRENT FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: US 60/208,063
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 54020
SEQ ID NO 51737
LENGTH: 590
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(590)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: LIB3637-255-Q6-K6-D10
US-09-865-419A-51737

Query Match 95.2%; Score 285.6; DB 33; Length 590;
Best Local Similarity 97.0%; Pred. No. 1.8e-82;
Matches 291; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 gattattgacacacccgctcctgctggtatgcatcatcaattgtcactagagacctg 60
|||
Db 81 gattattgacacacacgctcctgctggtatgcatcatcaattgtcactagagacctg 140
Qy 61 aactggaactactctctgtaattgcatcttcaagaagcgagacacactgaaccgca 120
|||
Db 141 aactggaactactctctgtaattgcatcttcaagaagcgagacacactgaaccgca 200
Qy 121 atggtctactagaatgacagaagccttcagagatcggtggtcgaattctcgaacaag 180
|||
Db 201 atggtctactagaatgacagaagccttcagagatcggtggtcgaattctcgaacaag 260
Qy 181 gtgtgcaattcactcaagaanaattctctgttgatacaactgctagatagagggatgt 240
|||
Db 261 gtgtgcaattcactcaagaanaattctctgttgatacaactgctagatagagggatgt 320
Qy 241 tagctcggttccctatgtttgattggtgtgtgtgtagagacttcagaanaatgtctgtgtg 300
|||
Db 321 tagctcggttccctatgtttgattggtgtgtgtgtagagacttcagaanaatgtctgtgtg 380

RESULT 12
US-09-654-617-388605
Sequence 388605, Application US/09654617
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jindong
TITLE OF INVENTION: Annotated Plant Genes
FILE REFERENCE: 38-21(15097)D
CURRENT APPLICATION NUMBER: US/09/654,617
CURRENT FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 463173
SEQ ID NO 388605
LENGTH: 1056
TYPE: DNA
ORGANISM: Oryza sativa
US-09-654-617-388605

Query Match 74.6%; Score 223.8; DB 25; Length 1056;
Best Local Similarity 88.4%; Pred. No. 4.2e-62;
Matches 243; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 26 tgggattgcatcaaatgtctcaactagaccctgaactggaactctgttaattgt 85
|||
Db 1 tgggattgcatcaaatgtctcaactagaccctgaactggaactctgttaattgt 60
Qy 86 catctctaagagcgagagacacactgaaccgcaatggtctactagaagtacagaagaagc 145
|||
Db 61 catctctaagagcgagagacacactgaaccgcaatggtctactagaagtacagaagaagc 120
Qy 146 ctccagagatcggtggtcgaattctcgaacaaggtgtgtgcaattactcaagaanaatc 205
|||
Db 121 ctccagagatcggtggtcgaattctcgaacaaggtgtgtgcaattactcaagaanaatc 180
Qy 206 tctgttgataaactgtctagatagagagatgttagctggttccctactgttgatgt 265
|||
Db 181 tctgttgataaactgtctagatagagagatgttagctggttccctactgttgatgt 240
Qy 266 ggtgtgtgtagacttcagaanaatgtctgtgtg 300
|||
Db 241 ggtgtgtgtagacttcagaanaatgtctgtgtg 275

RESULT 13
US-09-684-016-388605
Sequence 388605, Application US/09684016
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jindong
TITLE OF INVENTION: Annotated Plant Genes
FILE REFERENCE: 38-21(15097)D
CURRENT APPLICATION NUMBER: US/09/684,016

Query Match	74.68;	Score 223.8;	DB 27;	Length 1056;
Best Local Similarity	88.48;	Pred. No. 4.2e-62;		
Matches 243; Conservative	0;	Mismatches 32;	Indels 0;	Gaps 0;

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RESULT 14
US-09-849-529A-21745
: Sequence: 21745, Application US/09849529A
: GENERAL INFORMATION:
: APPLICANT: Fincher, Karen L.
: TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
: TITLE OF INVENTION: Plants
: FILE REFERENCE: 38-21(51893)B
: CURRENT APPLICATION NUMBER: US/09/849,529A
: PRIORITY FILING DATE: 2001-05-07
: PRIOR APPLICATION NUMBER: US 60/196,868
: PRIORITY FILING DATE: 2000-05-09
: NUMBER OF SEQ ID NOS: 24076
: SEQ ID NO 21745
: LENGTH: 509
: TYPE: DNA
: ORGANISM: Gossypium hirsutum
: FEATURE:
: OTHER INFORMATION: Clone ID: LIB585-052-P1-K1-C6
: US-09-849-529A-21745

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	Query March	72.8%	Score 218.4;	DB 32;	Length 509;
	Best Local Similarity	83.0%;	Pred. No. 1.86-60;		
	Matches 249; Conservative	0;	Mismatches 51;	Indels 0;	Gaps 0;
OY	1 gattatctgcaacaccgcgtcctcgctggatgatcatcacaattgtcctaactgagacctg	60			
Dd	71 gatctatcgataataacagatccctgctggaaatcgatcatcacatagacacaactctggccctg	130			
OY	61 aacgcgaacaaatccttgcfaatgcatttttaagaaggagggagacaccctgaaaccgca	120			
Dd	131 agtggtccttactcctcttgaattcgattttaaagaagtggagggafaccccctgaaacaaga	190			
OY	121 atgctcactagaagtagacagaagccttcagagatgtggcgctfccaattcttcgaaacag	180			

Db 191 atgttcattggaagfacagaagaagcttcgcgtgaagctggtcttgatttcgaacaacag 250

Oy 181 gtgttcgaattactcaagaanaattctcgtgttgataaacctctggaataagagatgc 240

Db 251 gtgtgtctataacacagaagaattctctgttgtaacaacctgcgaagatcgaggttcggg 310

Oy 241 taactcgggtctctctgtgttgatgggtttgggttgtagactcaagaatgtctgcctgg 300

Db 311 tagcaagttctccctatgtttgattcgggtctgggtgcagagacctctgaatgtctcattg 370

```

RESULT      15
US-60-196-868-21723
: Sequence 21723, Application US/60196868
: GENERAL INFORMATION:
: APPLICANT: Fincher, Karen L.
: APPLICANT: McCarter, David W.
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
: TITLE OF INVENTION: PLANTS
: FILE REFERENCE: 38-21(51893)A
: CURRENT APPLICATION NUMBER: US/60/196,868
: CURRENT FILING DATE: 2000-05-09
: NUMBER OF SEQ ID NOS: 24054
: SEQ ID NO 21723
: LENGTH: 509
: TYPE: DNA
: ORGANISM: Gossypium hirsutum
: OTHER INFORMATION: Clone ID: LIB3585-052-P1-K1-C6
US-60-196-868-21723

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Query Match	72.8%	Score 218.4	DB 58	Length 509
Best Local Similarity	83.0%	Pred. No. 1.8e-60		
Matches 24/9	Conservative 0	Mismatches 51	Indels 0	Gaps 0
QY	1 gattttttacacacacgcgactcctctggtgattgatacatacaaatgtctcaactaggaactg 60			
Db	71 gattttttatataataagaatccctgctggaatgatgatacataatagacaacttggcctg 130			
QY	61 aactggacaactactcttgaatctgcattcttccaaagaagggagacacactgaaacccgca 120			
Db	131 agttggctctactactcttgaatctgattcgattccaagaagaggagggagcaaccttgaacaagaa 190			
QY	121 atgtgtactatagaagtacagaagaagccttcagagatgcgggctgtgcaattcttcgaacaagg 180			
Db	191 atggctcatcttgaaagatcacagaagaagccttcgtagaagctgtgcatcttgcaacaacagg 250			
QY	181 gttgttcgaattactcaagaanaattctctgttcgtaataacagtcagagatagagagattgt 240			
Db	251 gttgttcgaataacacaagaanaattcttgttcgacaacactgcgaagattgaggtttggg 310			
QY	241 tagctcgagttctcctatgttttgaatggtgtgtgtgttaagacttcaagaatgtctgcgtgtg 300			
Db	311 tagccaagttccctactgttcttcatatgggtgttcggacagaccttcgaatgtctgcgcagttg 370			

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Search completed: July 3, 2002, 11:18:17
Job time: 34846 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 3, 2002, 08:11:53 ; Search time 185.98 seconds
(without alignments)
396.226 Million cell updates/sec

Title: US-09-300-482-619

Perfect score: 300
Sequence: 1 gattattgacaacacgat.....ttcagaatgtctgtgtg 300

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/lna/5A.COMB.seq:*
2: /cgn2_6/ptodata/2/lna/5B.COMB.seq:*
3: /cgn2_6/ptodata/2/lna/6A.COMB.seq:*
4: /cgn2_6/ptodata/2/lna/6B.COMB.seq:*
5: /cgn2_6/ptodata/2/lna/PCITUS.COMB.seq:*
6: /cgn2_6/ptodata/2/lna/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	30.6	10.2	1051	3	US-08-961-083-125
C 2	29.8	9.9	1750	3	US-08-859-167-1
C 3	29.8	9.9	1750	3	US-09-109-273-1
C 4	29.8	9.9	1750	4	US-09-276-993-1
C 5	29.8	9.9	2040	4	US-09-069-023-33
C 6	29.8	9.9	2045	4	US-08-484-493-1
C 7	29.8	9.9	2297	1	US-08-484-493-1
C 8	29.8	9.9	2297	1	US-08-484-494-1
C 9	29.8	9.9	2297	2	US-08-345-212-1
C 10	29.8	9.9	2297	3	US-09-249-003-1
C 11	29.8	9.9	4428	1	US-08-484-493-6
C 12	29.8	9.9	4428	2	US-08-484-494-6
C 13	29.8	9.9	4428	2	US-08-345-212-6
C 14	29.8	9.9	4428	3	US-09-249-003-6
C 15	28.2	9.4	4546	4	US-09-134-218-2
C 16	28.2	9.3	1932	3	US-08-714-918-97
C 17	28.2	9.3	1932	4	US-09-265-315-97
C 18	28.2	9.3	1932	4	US-09-265-315-97
C 19	28.2	9.3	1932	4	US-09-265-417-97
C 20	28.2	9.3	15225	2	US-08-892-403A-2
C 21	27.6	9.2	1146	1	US-08-487-810-1
C 22	27.6	9.2	3906	2	US-08-469-537A-102
C 23	27.6	9.2	4165	1	US-08-442-248-1
C 24	27.6	9.2	4165	1	US-08-440-815-1
C 25	27.6	9.2	4165	4	US-08-486-448-1
C 26	27.4	9.1	351	4	US-09-660-877-17
C 27	27.4	9.1	1055	1	US-08-618-464-1

C 28	27.4	9.1	1055	3	US-09-107-615-1	Sequence 1, Appl
C 29	27.4	9.1	1055	5	PCT-US95-04896-1	Sequence 1, Appl
C 30	27.4	9.1	1881	4	US-09-553-498-1	Sequence 1, Appl
C 31	27.4	9.1	1881	4	US-09-553-498-3	Sequence 3, Appl
C 32	26.8	8.9	2441	1	US-08-332-312-1	Sequence 1, Appl
C 33	26.8	8.9	2624	1	US-08-032-382B-1	Sequence 1, Appl
C 34	26.8	8.9	3705	5	PCT-US96-03940-7	Sequence 7, Appl
C 35	26.8	8.9	5648	5	PCT-US96-03940-1	Sequence 1, Appl
C 36	26.6	8.9	1426	4	US-08-858-207A-78	Sequence 78, Appl
C 37	26.4	8.8	665	2	US-08-980-060-12	Sequence 12, Appl
C 38	26.4	8.8	665	4	US-09-307-185-12	Sequence 12, Appl
C 39	26.4	8.8	1236	4	US-09-445-472-2	Sequence 2, Appl
C 40	26.4	8.8	1566	4	US-08-894-818B-4	Sequence 4, Appl
C 41	26.4	8.8	1806	2	US-08-980-060-1	Sequence 1, Appl
C 42	26.4	8.8	1806	4	US-09-307-185-1	Sequence 1, Appl
C 43	26.4	8.8	1962	4	US-08-894-818B-34	Sequence 34, Appl
C 44	26.4	8.8	1962	4	US-09-445-472-15	Sequence 15, Appl
C 45	26.4	8.8	3089	1	US-07-921-796-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-08-961-083-125/c
Sequence 125, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigen and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 125:
SEQUENCE CHARACTERISTICS:
LENGTH: 1051 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-083-125

Query Match 10.2%; Score 30.6; DB 3; Length 1051;
Best Local Similarity 53.8%; Pred. No. 0.78;
Matches 63; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 12 aaacacgacatcgtcgtggtatgataatgaccccaactgagactggaactggaact 71
DB 677 AACCCACATCCCTTCTGCATGACGACAGGAGGTAATCTTCATCTTCTGCGCAACTGAT 618


```

; TITLE OF INVENTION: OF MAKING THE SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6207801-1
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/276,993
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,167
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1750 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 413..1750
; US-09-276-993-1

Query Match
Best Local Similarity 9.9%; Score 29.8; DB 4; Length 1750;
Matches 70; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 54 gacactgaactggcaactactctgtatgtcttaagagcgagcacaccctgaa 113
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 365 GGAGCTGTACTGCAAGACCCTTGAGCTTCCCTAGCTAAGACTAGAGTGTCTGCGAA 424

QY 114 acccgcaatggtctactagaagtaacaaagccctcagagatcggggctgcaattctcg 173
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 425 GTCATCCATCAGGTTGAAGACCTTGATACAGATGAGAGGAGATGCTCTTTTGG 484

QY 174 aaacagggtgtgcaat 190
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 485 TGCCGGAGTGTGCTAT 501

RESULT 5
US-09-069-023-33
; Sequence 33, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 33
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-069-023-33

Query Match
Best Local Similarity 9.9%; Score 29.8; DB 4; Length 2040;
Matches 70; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 54 gacactgaactggcaactactctgtatgtcttaagagcgagcacaccctgaa 113
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 388 ggagctgtaccgcaagacccttgagcttccacagcttaagatgaagatgtctgctgaa 447

QY 114 acccgcaatggtctactagaagtaacaaagccctcagagatcggggctgcaattctcg 173
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 448 gtcatcctacatcggttgaagaagcaccttgatcacatgaatgaagaagatgctgtcttttg 507

QY 174 aaacagggtgtgcaat 190
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 508 tgccggagatgtgctat 524

RESULT 6
US-08-795-088A-1
; Sequence 1, Application US/08795088A
; Patent No. 6242569
; GENERAL INFORMATION:
; APPLICANT: Sul, Hong-Bing
; APPLICANT: Goeddel, David V.
; TITLE OF INVENTION: Regulators of Apoptosis
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Science & Technology Law Group
; STREET: 75 Denise Drive
; CITY: Hillsborough
; STATE: California
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,088A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2045 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-795-088A-1

Query Match
Best Local Similarity 9.9%; Score 29.8; DB 4; Length 2045;
Matches 70; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 54 gacactgaactggcaactactctgtatgtcttaagagcgagcacaccctgaa 113
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 463 GGAGCTGTACTGCAAGACCCTTGAGCTTCCCTAGCTAAGACTAGAGTGTCTGCGAA 522
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```
RESULT 9
US-08-345-212-1
; Sequence 1, Application US/08345212
; Patent No. 5932211
; GENERAL INFORMATION:
; APPLICANT: Wilson, Peter J
; APPLICANT: Morris, Charles P
; APPLICANT: Anson, Donald S
; APPLICANT: Occhiodoro, Teresa
; APPLICANT: Bielicki, Julie
; APPLICANT: Clements, Peter R
; APPLICANT: Hopwood, John J
; TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
; TITLE OF INVENTION: IDURONATE 2-SULFATASE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/345,212
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 991,973
; FILING DATE: 17-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8416Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4366
; TELEFAX: 516-742-4343
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2297 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 125..1774
US-08-345-212-1

Query Match          9.7%; Score 29; DB 2; Length 2297;
Best Local Similarity 53.0%; Pred. No. 3.8;
Matches 62; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 121 atggtctactagaagtaacgaagaatctctgttgataatacaactgctaagaatagaagat 237
    || || || || || || || || || || || || || || || || || || || || || ||
DB 1505 ATTGCTATATAGCAGATATCCCGGCTTCAGACATCCCTCAGATGGAATTCGTGACAAGCCG 1564

QY 181 gtgtgcaattactcaagaanaattctctgttgataatacaactgctaagaatagaagat 237
    || || || || || || || || || || || || || || || || || || || || || ||
DB 1565 AGTTTAAAGATATTAAGATCATGGCTATTCATACGACCATATAGACTATAGGTAT 1621

RESULT 10
US-09-249-003-1
; Sequence 1, Application US/09249003
; Patent No. 6153188
; GENERAL INFORMATION:
```

```
; APPLICANT: Wilson, Peter J
; APPLICANT: Morris, Charles P
; APPLICANT: Anson, Donald S
; APPLICANT: Occhiodoro, Teresa
; APPLICANT: Bielicki, Julie
; APPLICANT: Clements, Peter R
; APPLICANT: Hopwood, John J
; TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
; TITLE OF INVENTION: IDURONATE 2-SULFATASE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/249,003
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/991,973
; FILING DATE: 17-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8416Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2297 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 125..1774
US-09-249-003-1

Query Match          9.7%; Score 29; DB 3; Length 2297;
Best Local Similarity 53.0%; Pred. No. 3.8;
Matches 62; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 121 atggtctactagaagtaacgaagaatctctgttgataatacaactgctaagaatagaagat 180
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QY 181 gtgtgcaattactcaagaanaattctctgttgataatacaactgctaagaatagaagat 237
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DB 1565 AGTTTAAAGATATTAAGATCATGGCTATTCATACGACCATATAGACTATAGGTAT 1621

RESULT 11
US-08-484-493-6
; Sequence 6, Application US/08484493
; Patent No. 5728381
; GENERAL INFORMATION:
; APPLICANT: Wilson, Peter J
; APPLICANT: Morris, Charles P
; APPLICANT: Anson, Donald S
; APPLICANT: Occhiodoro, Teresa
; APPLICANT: Bielicki, Julie
```

1	APPLICANT:	Cléments, Peter R
2	APPLICANT:	Hopwood, John J
3	TITLE OF INVENTION:	GLYCOSYLATION VARIANTS OF
4	TITLE OF INVENTION:	IDRONATE 2-SULFATASE
5	NUMBER OF SEQUENCES:	15
6	CORRESPONDENCE ADDRESS:	
7	ADDRESSEE:	Scully, Scott, Murphy & Presser
8	STREET:	400 Garden City Plaza
9	CITY:	Garden City
10	STATE:	New York
11	COUNTRY:	USA
12	ZIP:	11530
13	COMPUTER READABLE FORM:	
14	MEDIUM TYPE:	Floppy disk
15	COMPUTER:	IBM PC compatible
16	OPERATING SYSTEM:	PC-DOS/MS-DOS
17	SOFTWARE:	Patentin Release #1.0, Version #1.25
18	CURRENT APPLICATION DATA:	
19	APPLICATION NUMBER:	US/08/484,493
20	FILING DATE:	07-JUN-1995
21	CLASSIFICATION:	424
22	PRIOR APPLICATION DATA:	
23	APPLICATION NUMBER:	991,973
24	FILING DATE:	17-DEC-1992
25	ATTORNEY/AGENT INFORMATION:	
26	NAME:	Digitiglio, Frank S
27	REGISTRATION NUMBER:	31,346
28	REFERENCE/DOCKET NUMBER:	84162
29	TELECOMMUNICATION INFORMATION:	
30	TELEPHONE:	516-742-4343
31	TELEFAX:	516-742-4366
32	TELEX:	230 901 SANS UR
33	INFORMATION FOR SEQ ID NO:	6:
34	SEQUENCE CHARACTERISTICS:	
35	LENGTH:	4428 base pairs
36	TYPE:	nucleic acid
37	STRANDEDNESS:	double
38	TOPOLOGY:	linear
39	MOLECULE TYPE:	DNA (genomic)
40	FEATURE:	
41	NAME/KEY:	CDS
42	LOCATION:	332..434
43	FEATURE:	
44	NAME/KEY:	Intron
45	LOCATION:	536..537
46	FEATURE:	
47	NAME/KEY:	CDS
48	LOCATION:	693..829
49	FEATURE:	
50	NAME/KEY:	Intron
51	LOCATION:	962..963
52	FEATURE:	
53	NAME/KEY:	CDS
54	LOCATION:	1044..1221
55	FEATURE:	
56	NAME/KEY:	Intron
57	LOCATION:	1350..1351
58	FEATURE:	
59	NAME/KEY:	CDS
60	LOCATION:	1480..1569
61	FEATURE:	
62	NAME/KEY:	Intron
63	LOCATION:	1716..1717
64	FEATURE:	
65	NAME/KEY:	CDS
66	LOCATION:	1841..2041
67	FEATURE:	
68	NAME/KEY:	Intron
69	LOCATION:	2206..2207
70	FEATURE:	
71	NAME/KEY:	CDS
72	LOCATION:	2294..2464
73	FEATURE:	

?	NAME/KEY:	Intron
?	LOCATION:	2585..2588
?	FEATURE:	
?	NAME/KEY:	CDS
?	LOCATION:	2684..2810
?	FEATURE:	
?	NAME/KEY:	Intron
?	LOCATION:	2904..2905
?	FEATURE:	
?	NAME/KEY:	CDS
?	LOCATION:	3033..3206
?	FEATURE:	
?	NAME/KEY:	Intron
?	LOCATION:	3308..3309
?	FEATURE:	
?	NAME/KEY:	CDS
?	LOCATION:	3435..3908
US-08-464		-933-6

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Best Local Similarity 53.0%; Pred. No. 5.1;
Matches 62; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
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[illegible]

RESULT 12

US-08-484-494-6
; Sequence 6, Application US/08484494
; Patent No. 5708320

1 GENERAL INFORMATION:
2 APPLICANT: WILSON, Peter J
3 APPLICANT: Morris, Charles P
4 APPLICANT: Anson, Donald S
5 APPLICANT: Occhiodoro, Teresa
6 APPLICANT: Bielski, Julie
7 APPLICANT: Clements, Peter R
8 APPLICANT: Hopwood, John J
9 TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
10 TITLE OF INVENTION: IDURONATE 2-SULFATASE
11 NUMBER OF SEQUENCES: 15
12 CORRESPONDENCE ADDRESS:

ADDRESSEE: scully, scott, murphy & presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: USA
ORD. INFO

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,494
FILING DATE: 07-JUN-1995
CLASSIFICATION:

APPLICATION NUMBER: 991,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: DIGISLO, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8416Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343

FEATURE:
NAME/KEY: Intron
LOCATION: 1716..1717
FEATURE:
NAME/KEY: CDS
LOCATION: 1841..2041
FEATURE:
NAME/KEY: Intron
LOCATION: 2206..2207
FEATURE:
NAME/KEY: CDS
LOCATION: 2294..2464
FEATURE:
NAME/KEY: Intron
LOCATION: 2585..2586
FEATURE:
NAME/KEY: CDS
LOCATION: 2684..2810
FEATURE:
NAME/KEY: Intron
LOCATION: 2904..2905
FEATURE:
NAME/KEY: CDS
LOCATION: 3033..3206
FEATURE:
NAME/KEY: Intron
LOCATION: 3308..3309
FEATURE:
NAME/KEY: CDS
LOCATION: 3435..3908
US-08-345-212-6

Query Match
Best Local Similarity 9.7%; Score 29; DB 2; Length 4428;
Matches 62; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
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DB 3636 attgcctatagccagatgcccgccttcacagatccctcagtggaatttcgacacagccg 3635
QY 181 gtgttgcaattactcaagaanaattctctgttgataacactcgtcagaatagaggat 237
DB 3696 agtttaaaagatataaagatcattggcctatttcacatcgcacacatagactatagctat 3752

RESULT 14
US-09-249-003-6
Sequence 6, Application US/09249003
Patent No. 6153188
GENERAL INFORMATION:
APPLICANT: Wilson, Peter J
APPLICANT: Morris, Charles P
APPLICANT: Anson, Donald S
APPLICANT: Occhiodoro, Teresa
APPLICANT: Bielicki, Julie
APPLICANT: Hopwood, John R
TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,003
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/991,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Digilio, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 84162
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4428 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 332..434
FEATURE:
NAME/KEY: Intron
LOCATION: 536..537
FEATURE:
NAME/KEY: CDS
LOCATION: 693..829
FEATURE:
NAME/KEY: Intron
LOCATION: 962..963
FEATURE:
NAME/KEY: CDS
LOCATION: 1044..1221
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NAME/KEY: Intron
LOCATION: 1350..1351
FEATURE:
NAME/KEY: CDS
LOCATION: 1480..1569
FEATURE:
NAME/KEY: Intron
LOCATION: 1716..1717
FEATURE:
NAME/KEY: CDS
LOCATION: 1841..2041
FEATURE:
NAME/KEY: Intron
LOCATION: 2206..2207
FEATURE:
NAME/KEY: CDS
LOCATION: 2294..2464
FEATURE:
NAME/KEY: Intron
LOCATION: 2585..2586
FEATURE:
NAME/KEY: CDS
LOCATION: 2684..2810
FEATURE:
NAME/KEY: Intron
LOCATION: 2904..2905
FEATURE:
NAME/KEY: CDS
LOCATION: 3033..3206
FEATURE:
NAME/KEY: Intron
LOCATION: 3308..3309
FEATURE:
NAME/KEY: CDS
LOCATION: 3435..3908

US-09-249-003-6

Query Match	9.7%	Score 29;	DB 3;	Length 4428;
Best Local Similarity	53.0%;	Pred. No. 5.1;		
Matches	62;	Conservative	0;	Mismatches 55;
			Indels	0;
			Gaps	0;

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QY      121 atggtctactagaagtacagaaagccttcagagatcgggctgcattctcgaaacagg   180
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Db      3636 ATTGCGCTATTAGCCAGTATCCCCGCCCTTCACACATCCTCACTGGAA'TCTGCACAAGCG   3695
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Qy 181 ggtctgcattactcaagaataatcctctgttgataaacactgtaagaaatagaggat 237
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Db 3696 AGTTTAAAGATATAAAGCATGCGGTATTCCATACGCACCATAGACTATAGCTAT 3752

RESULT 15
 US-09-134-218-2/c
 : Sequence 2, Application US/09134218A
 : Patent No. 6312926
 : GENERAL INFORMATION:
 : APPLICANT: Shaktin, Aaron J.
 : APPLICANT: Pillutla, Renuka
 : APPLICANT: Reinberg, Danny
 : APPLICANT: Yu, Zheng
 : APPLICANT: Moldanado, Edlo
 : TITLE OF INVENTION: MRN CAPING ENZYMES AND USES THEREOF
 : FILE REFERENCE: 601-1-079 ss
 : CURRENT APPLICATION NUMBER: US/09/134,218A
 : CURRENT FILING DATE: 1998-08-14
 : NUMBER OF SEQ ID NOS: 19
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 2
 : LENGTH: 4546
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : US-09-134-218-2

Query Match	9.48;	Score 28.2;	DB 4;	Length 4546;
Best Local Similarity	48.48;	Pred. No. 9.4;		
Matches	78;	Conservative	0;	Mismatches 83;
			Indels	0;
			Gaps	0;

OY 134 agtcaagaaagccttcagagatgcggggtcgaattctcgaaacaggltgtlccaattac 193
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Db 3139 AGTTCCACAGATGCTACACTTTCGCCCTGCATTATCTACAGTGGAGACCATTTTC 3080

Qy 194 tcagaagaaatctcgtttgataaacactgctagaatagaggatgttgtagctggttcc 253
| | | | | | | | | | | | | | |
Db 3079 TGGTGCACGACATCTATTCCATGACATTACTTCATAACAAGAGTTAGCTGGCATTC 3020

Oy	254	tatgcttgattggattggtgtgtagactccgaatgtctg	294
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Search completed: July 3, 2002, 08:11:57
Job time: 25882 sec

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